

## BLAST Basic Local Alignment Search Tool

- Your search is limited to records matching entrez query: Homo sapiens [ORGN].

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### Protein Sequence (430 letters)

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

lcl|24806

#### Description

None

#### Molecule type

amino acid

#### Query Length

430

#### Database Name

nr

#### Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

#### Program

BLASTP 2.2.19+ Citation

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

#### Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

### Search Parameters

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Threshold	11
Composition-based stats	2
Filter string	F
Genetic Code	1
Window Size	40

### Database

Posted date	Feb 12, 2009 6:03 PM
Number of letters	2,713,143,868
Number of sequences	7,873,120
Entrez query	Homo sapiens [ORGN]

### Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.326046	0.267
K	0.138029	0.041
H	0.443787	0.14

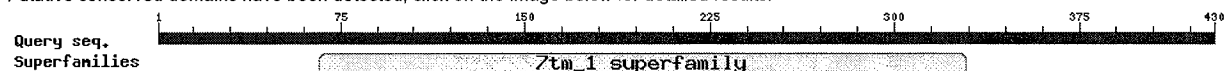
### Results Statistics

Length adjustment	115
Effective length of query	315
Effective length of database	54918291
Effective search space	17299261665
Effective search space used	17299261665

#### Graphic Summary

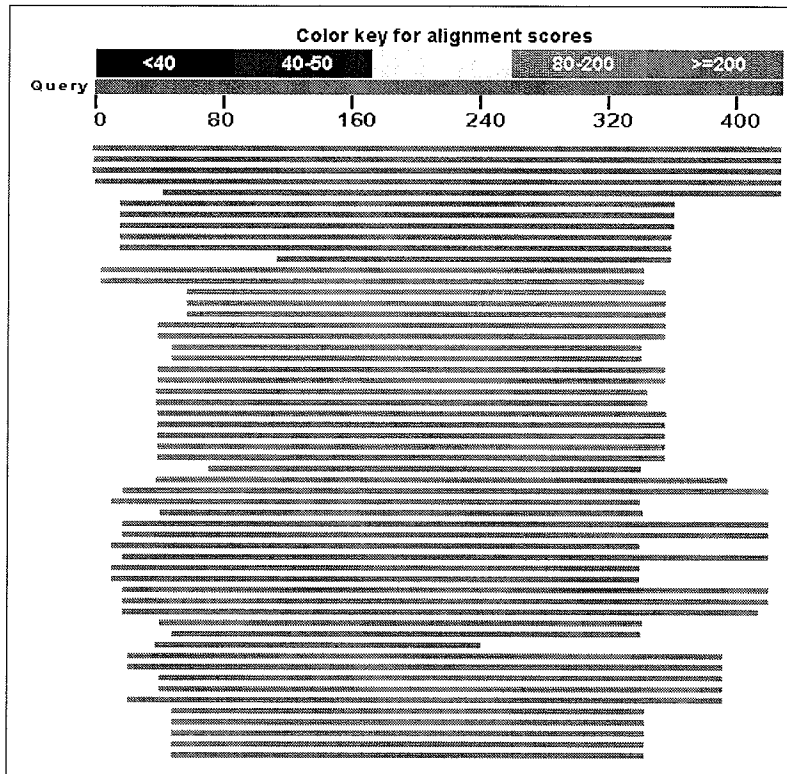
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



### Distribution of 104 Blast Hits on the Query Sequence

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



# Descriptions

Sequences producing significant alignments:	Score (Bits)	E Value	
ref NP_071429.1  neuro peptide FF receptor 1 [Homo sapiens] >s...	881	0.0	UG
dbj BAC05950.1  seven transmembrane helix receptor [Homo sapi...	880	0.0	G
gb AAK94199.1 AF330055_1 neuro peptide NPVF receptor [Homo sap...	880	0.0	G
emb CAI12599.1  neuro peptide FF receptor 1 [Homo sapiens]	877	0.0	G
gb EAW54387.1  neuro peptide FF receptor 1 [Homo sapiens]	789	0.0	G
ref NP_444264.1  neuro peptide FF receptor 2 isoform 2 [Homo s...	423	7e-118	UG
ref NP_001138228.1  neuro peptide FF receptor 2 isoform 3 [Hom...	422	1e-117	G
gb AAK58513.1 AF236083_1 G-protein-coupled receptor 74 [Homo ...	422	2e-117	G
gb AAD22047.1  G-protein-coupled receptor [Homo sapiens]	420	4e-117	G
ref NP_004876.2  neuro peptide FF receptor 2 isoform 1 [Homo s...	420	4e-117	G
gb EAX05647.1  neuro peptide FF receptor 2, isoform CRA_a [Hom...	286	1e-76	G
ref NP_001517.2  orexin receptor 2 [Homo sapiens] >sp O43614....	190	7e-48	G
gb AAC39602.1  orexin receptor-2; OX2R; G protein-coupled rec...	190	7e-48	G
gb AAC39601.1  orexin receptor-1; OX1R; G protein-coupled rec...	181	4e-45	G
ref NP_001516.2  orexin receptor 1 [Homo sapiens] >sp O43613....	179	2e-44	G
dbj BAF83210.1  unnamed protein product [Homo sapiens]	179	2e-44	G
ref NP_000901.1  neuro peptide Y receptor Y2 [Homo sapiens] >s...	167	9e-41	UG
gb AAA93170.1  type 2 neuro peptide Y receptor	165	3e-40	G
ref NP_937822.2  G protein-coupled receptor 103 [Homo sapiens...	165	3e-40	UG
dbj BAC98938.1  QRFP receptor [Homo sapiens]	164	4e-40	G
gb AAD00248.1  neuro peptide Y receptor type 2 [Homo sapiens]	164	5e-40	G
gb AAB07760.1  neuro peptide y/peptide YY receptor type 2	164	6e-40	G
gb AAA59920.1  neuro peptide y receptor	160	8e-39	G
ref NP_000900.1  neuro peptide Y receptor Y1 [Homo sapiens] >s...	160	1e-38	UG
gb AAF43705.1 AF236081_1 orphan G-protein coupled receptor GP...	156	1e-37	G
sp Q9NYM4.2 GPR83_HUMAN RecName: Full=Probable G-protein coup...	156	1e-37	G
ref NP_057624.2  G protein-coupled receptor 83 [Homo sapiens]...	156	1e-37	UG
dbj BAA96064.1  KIAA1540 protein [Homo sapiens]	156	1e-37	G
gb AAH67474.1  G protein-coupled receptor 83 [Homo sapiens]	152	2e-36	G
gb AAI28134.1  GPR103 protein [Homo sapiens]	149	2e-35	G
ref NP_003848.1  galanin receptor 2 [Homo sapiens] >sp O43603...	148	3e-35	UG
gb AAB05897.1  neurokinin-2 receptor	148	4e-35	G
gb AAH99637.1  Pancreatic polypeptide receptor 1 [Homo sapiens]	148	4e-35	G
ref NP_000721.1  cholecystokinin A receptor [Homo sapiens] >s...	147	8e-35	UG
sp P21452.2 NK2R_HUMAN RecName: Full=Substance-K receptor; Sh...	146	1e-34	G
gb AAC31760.1  neurokinin A receptor [Homo sapiens] >gb AAA60...	145	3e-34	G
ref NP_005963.3  pancreatic polypeptide receptor 1 [Homo sapi...	145	3e-34	UG
ref NP_001048.2  tachykinin receptor 2 [Homo sapiens] >dbj BA...	145	3e-34	UG
gb AAB07759.1  pancreatic polypeptide receptor >gb AAV68196.1...	145	3e-34	G
emb CAG46748.1  PPYR1 [Homo sapiens]	143	9e-34	G
gb EAW54325.1  tachykinin receptor 2, isoform CRA_b [Homo sap...	142	3e-33	G
gb AAH96842.1  Tachykinin receptor 2 [Homo sapiens]	140	9e-33	G
gb AAB20304.1  substance K receptor, SK receptor [human, Pep...	139	2e-32	G
prf 2118221A cholecystokinin A receptor	137	6e-32	G
gb AAL26488.1 AF411117_1 G protein-coupled receptor [Homo sap...	135	3e-31	G
dbj BAD92474.1  neuro peptide Y receptor Y1 variant [Homo sapi...	127	9e-29	G
gb AAI22552.1  Tachykinin receptor 3 [Homo sapiens]	125	2e-28	G
gb AAB21706.1  neurokinin-3 receptor; NK-3 receptor [Homo sap...	125	2e-28	G
emb CAA46291.1  neuromedin K receptor [Homo sapiens]	125	3e-28	G
ref NP_001050.1  tachykinin receptor 3 [Homo sapiens] >sp P29...	125	3e-28	UG
gb AAH95527.1  TACR3 protein [Homo sapiens]	124	7e-28	G
sp Q13585.1 MTR1L_HUMAN RecName: Full=Melatonin-related recep...	123	1e-27	G
ref NP_004215.2  G protein-coupled receptor 50 [Homo sapiens]	123	1e-27	UG
gb AAI03697.1  GPR50 protein [Homo sapiens] >gb AAI05684.1  G...	122	2e-27	G
gb AAI05685.1  G protein-coupled receptor 50 [Homo sapiens] >...	122	2e-27	G
gb EAW99402.1  G protein-coupled receptor 50 [Homo sapiens]	122	2e-27	G
ref NP_001718.1  bombesin-like receptor 3 [Homo sapiens] >sp ...	122	2e-27	UG
emb CAG46720.1  DRD1 [Homo sapiens]	122	2e-27	G
ref NP_001471.2  galanin receptor 1 [Homo sapiens]	122	2e-27	UG
sp P47211.1 GALR1_HUMAN RecName: Full=Galanin receptor type 1...	122	2e-27	G
emb CAA41734.1  D-1 dopamine receptor [Homo sapiens]	122	2e-27	G
gb AAK83235.1 AF343725_1 G-protein-coupled receptor GPR54 [Ho...	122	2e-27	G

gb EAW61376.1	dopamine receptor D1, isoform CRA_a [Homo sapiens]	122	2e-27	<b>G</b>
ref NP_000785.1	dopamine receptor D1 [Homo sapiens] >sp P217...	122	2e-27	<b>UG</b>
gb AAB60356.1	galanin receptor >gb AAC95397.1  galanin recep...	122	3e-27	<b>G</b>
ref NP_115940.2	G protein-coupled receptor 54 [Homo sapiens]...	122	3e-27	<b>UG</b>
prf  1614340A	dopamine receptor D1	120	6e-27	
dbj BAG36078.1	unnamed protein product [Homo sapiens]	117	5e-26	<b>G</b>
ref NP_001041.1	somatostatin receptor 2 [Homo sapiens] >sp P...	117	8e-26	<b>UG</b>
gb AAA20828.1	somatostatin receptor	117	8e-26	<b>G</b>
ref NP_001044.1	somatostatin receptor 5 [Homo sapiens] >sp P...	117	9e-26	<b>UG</b>
ref NP_004239.1	G protein-coupled receptor 10 [Homo sapiens]...	117	9e-26	<b>UG</b>
gb AAF42810.1	AF184174_2 somatostatin receptor 2B [Homo sapie...	116	1e-25	<b>G</b>
ref NP_658986.1	prokineticin receptor 2 [Homo sapiens] >sp Q...	116	1e-25	<b>UG</b>
gb EAX10422.1	prokineticin receptor 2 [Homo sapiens]	116	2e-25	<b>G</b>
dbj BAG36594.1	unnamed protein product [Homo sapiens]	116	2e-25	<b>G</b>
gb AAH95542.1	Neuromedin B receptor [Homo sapiens]	115	2e-25	<b>G</b>
gb ABQ52418.1	prokineticin receptor 2 [Homo sapiens]	115	2e-25	<b>G</b>
ref NP_002502.2	neuromedin B receptor [Homo sapiens] >sp P28...	115	3e-25	<b>UG</b>
gb AAA59939.1	neuromedin B receptor >gb AAB27330.1  neuromed...	115	3e-25	<b>G</b>
gb AAA36623.1	somatostatin receptor >dbj BAA04106.1  fourth ...	115	4e-25	<b>G</b>
gb AAK61266.1	AE006466_1 somatostatin receptor type 5 [Homo s...	115	4e-25	<b>G</b>
ref NP_005950.1	melatonin receptor 1B [Homo sapiens] >sp P49...	114	6e-25	<b>UG</b>
gb AAH09522.1	AAH09522 Unknown (protein for IMAGE:3354783) [H...	114	9e-25	<b>G</b>
ref NP_001043.2	somatostatin receptor 4 [Homo sapiens] >sp P...	113	1e-24	<b>UG</b>
gb AAN87342.1	DRG kappa 1 splice variant KOR 1A [Homo sapiens]	113	1e-24	<b>G</b>
gb EAX10169.1	somatostatin receptor 4, isoform CRA_b [Homo s...	113	1e-24	<b>G</b>
emb CAH73066.1	prolactin releasing hormone receptor [Homo sa...	113	1e-24	<b>G</b>
dbj BAF82684.1	unnamed protein product [Homo sapiens]	113	1e-24	<b>G</b>
gb AAA60565.1	somatostatin receptor	112	2e-24	<b>G</b>
dbj BAG60542.1	unnamed protein product [Homo sapiens]	110	6e-24	<b>G</b>
gb AAM21070.1	AF498922_1 opioid receptor kappa [Homo sapiens]...	110	6e-24	<b>G</b>
ref NP_000903.2	opioid receptor, kappa 1 [Homo sapiens] >sp ...	110	7e-24	<b>UG</b>
gb AAN32829.1	AF441129_1 cholecystokinin-C receptor [Homo sap...	110	8e-24	<b>G</b>
gb EAW68734.1	cholecystokinin B receptor, isoform CRA_a [Hom...	110	1e-23	<b>G</b>
gb EAX05261.1	G protein-coupled receptor 103, isoform CRA_a ...	110	1e-23	<b>G</b>
ref NP_795344.1	cholecystokinin B receptor [Homo sapiens] >s...	110	1e-23	<b>UG</b>
gb AAB30766.2	cholecystokinin B receptor [Homo sapiens]	109	1e-23	<b>G</b>
ref NP_001040.1	somatostatin receptor 1 [Homo sapiens] >sp P...	109	1e-23	<b>UG</b>
gb EAW68735.1	cholecystokinin B receptor, isoform CRA_b [Hom...	109	2e-23	<b>G</b>

Alignments Select All Get selected sequences Distance tree of results

```

>ref|NP_071429.1| UG neuropeptide FF receptor 1 [Homo sapiens]
  sp|Q9GZQ6.1|NPFF1_HUMAN G RecName: Full=Neuropeptide FF receptor 1; AltName: Full=G-protein
  coupled receptor 147; AltName: Full=RFamide-related peptide
  receptor OT7T022
  gb|AAG41397.1|AF268898_1 G neuropeptide FF receptor 1 [Homo sapiens]
  dbj|BAB17677.1| G RFamide-related peptide receptor [Homo sapiens]
  gb|AAI31581.1| G Neuropeptide FF receptor 1 [Homo sapiens]
  gb|ABY87927.1| G neuropeptide FF receptor 1 [Homo sapiens]
Length=430

  GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]
  (10 or fewer PubMed links)

  Score = 881 bits (2276), Expect = 0.0, Method: Compositional matrix adjust.
  Identities = 430/430 (100%), Positives = 430/430 (100%), Gaps = 0/430 (0%)

Query 1      MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVG 60
Sbjct 1      MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVG 60

Query 61     NTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGFICMPTTLVDNLITGWPFDNATCKMSG 120
Sbjct 61     NTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGFICMPTTLVDNLITGWPFDNATCKMSG 120


Query 121    LVQGMVSASVFTLVAIAVERFRCIVHPPREKLTLRKALVTIAVIWALALLIMCPSAVTL 180
Sbjct 121    LVQGMVSASVFTLVAIAVERFRCIVHPPREKLTLRKALVTIAVIWALALLIMCPSAVTL 180

Query 181    TVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIA 240
Sbjct 181    TVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIA 240

Query 241    RKLQAPGAPGAPGEGEADPRASRRRARVHMLVMVALFFTLISWLPWALLLLIDYGQLSA 300
Sbjct 241    RKLQAPGAPGAPGEGEADPRASRRRARVHMLVMVALFFTLISWLPWALLLLIDYGQLSA 300

```


Query	301	PQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAY	360
Sbjct	301	PQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAY	360
Query	361	SERPGLLHRRVVFVVVRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSH	420
Sbjct	361	SERPGLLHRRVVFVVVRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSH	420
Query	421	LPLTIPAWDI	430
Sbjct	421	LPLTIPAWDI	430

>dbj|BAC05950.1|  seven transmembrane helix receptor [Homo sapiens]  
Length=441

GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 880 bits (2274), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 429/429 (100%), Positives = 429/429 (100%), Gaps = 0/429 (0%)


Query	2	EGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGN	61
Sbjct	13	EGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGN	72
Query	62	TLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSG	121
Sbjct	73	TLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSG	132
Query	122	VQGMVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLT	181
Sbjct	133	VQGMVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLT	192
Query	182	VTREHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIAR	241
Sbjct	193	VTREHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIAR	252
Query	242	KLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYGQLSAP	301
Sbjct	253	KLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYGQLSAP	312
Query	302	QLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYS	361
Sbjct	313	QLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYS	372
Query	362	ERPGLLHRRVVFVVVRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSHL	421
Sbjct	373	ERPGLLHRRVVFVVVRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSHL	432
Query	422	PLTIPAWDI	430
Sbjct	433	PLTIPAWDI	441

>gb|AAK94199.1|AF330055\_1  neuropeptide NPVF receptor [Homo sapiens]  
Length=430

GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 880 bits (2273), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 429/430 (99%), Positives = 429/430 (99%), Gaps = 0/430 (0%)

Query	1	MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVG	60
Sbjct	1	MEGEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVG	60
Query	61	NLTVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSG	120
Sbjct	61	NLTVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSG	120
Query	121	LVQGMVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTL	180
Sbjct	121	LVQGMVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTL	180
Query	181	TVTREHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIA	240
Sbjct	181	TVTREHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIA	240
Query	241	RKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYGQLSA	300
Sbjct	241	RKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYGQLSA	300
Query	301	PQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAY	360
Sbjct	301	PQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAY	360
Query	361	SERPGLLHRRVVFVVVRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSH	420
Sbjct	361	SERPGLLHRRVVFVVVRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPGCSH	420
Query	421	LPLTIPAWDI	430
Sbjct	421	LPLTIPAWDI	430

>emb|CAI12599.1|  neuropeptide FF receptor 1 [Homo sapiens]  
Length=428

GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 877 bits (2265), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 428/428 (100%), Positives = 428/428 (100%), Gaps = 0/428 (0%)

Query	3	GEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNT	62
		GEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNT	

Sbjct	1	GEPSQPPNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNT	60
Query	63	LVCFIVLKNRHMHTVTNMFILNLAVSDLLVGI FCMPTTLVDNLITGWPF DNATCKMSGLV	122
Sbjct	61	LVCFIVLKNRHMHTVTNMFILNLAVSDLLVGI FCMPTTLVDNLITGWPF DNATCKMSGLV	120
Query	123	QGMSSVASVFTLVIAVERFRCIVHPFREKLT LRKALVTIAVIWALALLIMCPSAVTLTV	182
Sbjct	121	QGMSSVASVFTLVIAVERFRCIVHPFREKLT LRKALVTIAVIWALALLIMCPSAVTLTV	180
Query	183	TREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLF SHIYLAPLALIVVMYARIARK	242
Sbjct	181	TREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLF SHIYLAPLALIVVMYARIARK	240
Query	243	LCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTL SWLPLWALLLLIDYGQLSAPQ	302
Sbjct	241	LCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTL SWLPLWALLLLIDYGQLSAPQ	300
Query	303	LHLVTVYAFPPAHWLAFNSSANPIIYG YFNENFRRGFQA AFRARLCPRPSGSHKEAYSE	362
Sbjct	301	LHLVTVYAFPPAHWLAFNSSANPIIYG YFNENFRRGFQA AFRARLCPRPSGSHKEAYSE	360
Query	363	RPGGLLHRRVVFVVVRPSDSGLPSESGPSSGAPRGR LPLRNGRVAHGLPREGPGCSHLP	422
Sbjct	361	RPGGLLHRRVVFVVVRPSDSGLPSESGPSSGAPRGR LPLRNGRVAHGLPREGPGCSHLP	420
Query	423	LTIPAWDI 430	
Sbjct	421	LTIPAWDI 428	

>gb|EAW54387.1| **G** neuropeptide FF receptor 1 [Homo sapiens]  
Length=386

GENE ID: 64106 NPFFR1 | neuropeptide FF receptor 1 [Homo sapiens]  
(10 or fewer PubMed links)

Score = 789 bits (2037), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 386/386 (100%), Positives = 386/386 (100%), Gaps = 0/386 (0%)

Query	45	MFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGI FCMPTTLVDN	104
Sbjct	1	MFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGI FCMPTTLVDN	60
Query	105	LITGWPF DNATCKMSGLVQGMSSVASVFTLVIAVERFRCIVHPFREKLT LRKALVTIAV	164
Sbjct	61	LITGWPF DNATCKMSGLVQGMSSVASVFTLVIAVERFRCIVHPFREKLT LRKALVTIAV	120
Query	165	IWALALLIMCPSAVTLTVT TREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLF SHI	224
Sbjct	121	IWALALLIMCPSAVTLTVT TREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLF SHI	180
Query	225	YLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTL SWL	284
Sbjct	181	YLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTL SWL	240
Query	285	PLWALLLLIDYGQLSAPQLHLVTVYAFPPAHWLAFNSSANPIIYG YFNENFRRGFQA AF	344
Sbjct	241	PLWALLLLIDYGQLSAPQLHLVTVYAFPPAHWLAFNSSANPIIYG YFNENFRRGFQA AF	300
Query	345	RARLCPRPSGSHKEAYSERPGGLLHRRVVFVVVRPSDSGLPSESGPSSGAPRGR LPLRNG	404
Sbjct	301	RARLCPRPSGSHKEAYSERPGGLLHRRVVFVVVRPSDSGLPSESGPSSGAPRGR LPLRNG	360
Query	405	RVAHHGLPREGPGCSHLP LTIPAWDI 430	
Sbjct	361	RVAHHGLPREGPGCSHLP LTIPAWDI 386	

>ref|NP\_444264.1| **UG** neuropeptide FF receptor 2 isoform 2 [Homo sapiens]  
gb|AAF87078.1|AF257210\_1 **G** G-protein coupled receptor HLWAR77 [Homo sapiens]  
gb|AAG41398.1|AF268899\_1 **G** neuropeptide FF receptor 2 [Homo sapiens]  
gb|AAK94197.1|AF330053\_1 **G** neuropeptide NPFF receptor [Homo sapiens]  
gb|EAX05648.1| **G** neuropeptide FF receptor 2, isoform CRA\_b [Homo sapiens]  
gb|AAI13714.2| **G** Neuropeptide FF receptor 2 [Homo sapiens]  
gb|AAI01637.1| **G** Neuropeptide FF receptor 2 [Homo sapiens]  
dbj|BAF83626.1| **G** unnamed protein product [Homo sapiens]  
Length=420

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 423 bits (1087), Expect = 7e-118, Method: Compositional matrix adjust.  
Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)

Query	18	NGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTV	77
Sbjct	20	N T N+T+ +YY H VAA+FI++Y LIF LCM+GNT+VC FIV++N+HMHTV	79
Query	78	TNMFILNLAVSDLLVGI FCMPTTLVDNLITGWPF DNATCKMSGLVQGMSSVASVFTLVIAI	137
Sbjct	80	TN+FILNLA+SDLLVGI FCMPT TL+DN+I GWPF N CK+SGLVQG+SV+ASVFTLVIAI	139
Query	138	AVERFRCIVHPFREKLT LRKALVTIAVIWALALLIMCPSAVTLTVT TREEHHFM-VDARNR	196
Sbjct	140	AV+RF+C+V+PF+ KLT++ A V I +IW LA+ IM PSAV L V E+++ + +++N+	199
Query	197	SYPLYSCEAWPEKGMRRVYTTVLF SHIYLAPLALIVVMYARIARKLCQAPGPAPGGEEA	256
Sbjct	200	+ P+Y C E WP + MR++YTTVLF++IYLAPL+LIV+MY RI L +A P E +	259
Query	257	ADPR-ASRRRARVVHMLVMVALFFTL SWLPLWALLLLIDYGQLSAPQLHLVTVYAFPPAH	315
Sbjct	260	SR++ +++ ML++VAL F LSWLPLW L++L DY LS +L ++ +Y +PPAH	319

Query 316 WLAFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYSER 363  
WLAFF NSS NPIIYG+FNENFRRGFQ AF+ +LC + + EAY+ +  
Sbjct 320 WLAFGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKP-MEAYALK 366

>ref|NP\_001138228.1| **G** neuropeptide FF receptor 2 isoform 3 [Homo sapiens]  
gb|EAX05650.1| **G** neuropeptide FF receptor 2, isoform CRA\_d [Homo sapiens]  
Length=423

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 422 bits (1085), Expect = 1e-117, Method: Compositional matrix adjust.  
Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)

Query 18 NGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTV 77  
N T N+T+ +YY H VAA+FI++Y LIF LCM+GNT+VCFIV++N+HMHTV  
Sbjct 23 NDTKHHLYSDINITYVNYLHQPVAAIFIIISYFLIFFLCMMGNTVVCFIVMRNKHMTV 82

Query 78 TNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMSGVLVQGMVSASVFTLVAI 137  
TN+FILNLA+SDLLVGIFCMP TL+DN+I GWPF N CK+SGLVQG+SV+ASVFTLVAI  
Sbjct 83 TNLFILNLAISDLLVGIFCMPITLLDNIIAGWPPGNTMCKISGLVQGISVAASVFTLVAI 142

Query 138 AVERFRICIVHPFREKLTIRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFM-VDARNR 196  
AV+RF+C+V+PF+ KLT++ A V I +IW LA+ IM PSAV L V E+++ + +++N+  
Sbjct 143 AVDRFQCVCVYFPKPKLTIKTAFVIIMIIWLAITIMSPSAVMLHVQEEKYRVRLNSQNK 202

Query 197 SYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVMYARIARKLCQAPGPAPGGEEA 256  
+ P+Y C E WP + MR++YTTVLF++IYLAPL+LIV+MY RI L +A P G +  
Sbjct 203 TSPVYWCREDDWPNQEMRKIYTTVLFANIIYLAPLSLIVIMYGRIGISLFRAAVPHTGRKNQ 262

Query 257 ADPR-ASRRRARVHMLVMVALFFTLSWLPLWALLLLIDYQLSAPQLHLVTVYAFPPAH 315  
SR++ +++ ML++VAL F LSWLPLW L++L DY LS +L ++ +Y +PPAH  
Sbjct 263 EQWHVVSRRKKQIKMLLIALLFILSWLPLWLTMLLSYADLSPNELQIINIYIYPPAH 322

Query 316 WLAFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYSER 363  
WLAFF NSS NPIIYG+FNENFRRGFQ AF+ +LC + + EAY+ +  
Sbjct 323 WLAFGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKP-MEAYALK 369

>gb|AAK58513.1|AF236083\_1 **G** G-protein-coupled receptor 74 [Homo sapiens]  
Length=408

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 422 bits (1084), Expect = 2e-117, Method: Compositional matrix adjust.  
Identities = 197/348 (56%), Positives = 265/348 (76%), Gaps = 3/348 (0%)

Query 18 NGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTV 77  
N T N+T+ +YY H VAA+FI++Y LIF LCM+GNT+VCFIV++N+HMHTV  
Sbjct 23 NDTKHHLYSDINITYVNYLHQPVAAIFIIISYFLIFFLCMMGNTVVCFIVMRNKHMTV 82

Query 78 TNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMSGVLVQGMVSASVFTLVAI 137  
TN+FILNLA+SDLLVGIFCMP TL+DN+I GWPF N CK+SGLVQG+SV+ASVFTLVAI  
Sbjct 83 TNLFILNLAISDLLVGIFCMPITLLDNIIAGWPPGNTMCKISGLVQGISVAASVFTLVAI 142

Query 138 AVERFRICIVHPFREKLTIRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFM-VDARNR 196  
AV+RF+C+V+PF+ KLT++ A V I +IW LA+ IM PSAV L V E+++ + +++N+  
Sbjct 143 AVDRFQCVCVYFPKPKLTIKTAFVIIMIIWLAITIMSPSAVMLHVQEEKYRVRLNSQNK 202

Query 197 SYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVMYARIARKLCQAPGPAPGGEEA 256  
+ P+Y C E WP + MR++YTTVLF++IYLAPL+LIV+MY RI L +A P G +  
Sbjct 203 TSPVYWCREDDWPNQEMRKIYTTVLFANIIYLAPLSLIVIMYGRIGISLFRAAVPHTGRKNQ 262

Query 257 ADPR-ASRRRARVHMLVMVALFFTLSWLPLWALLLLIDYQLSAPQLHLVTVYAFPPAH 315  
SR++ +++ ML++VAL F LSWLPLW L++L DY LS +L ++ +Y +PPAH  
Sbjct 263 EQWHVVSRRKKQIKMLLIALLFILSWLPLWLTMLLSYADLSPNELQIINIYIYPPAH 322

Query 316 WLAFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYSER 363  
WLAFF NSS NPIIYG+FNENFRRGFQ AF+ +LC + + EAY+ +  
Sbjct 323 WLAFGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKP-MEAYTLK 369

>gb|AAD22047.1| **G** G-protein-coupled receptor [Homo sapiens]  
Length=522

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 420 bits (1080), Expect = 4e-117, Method: Compositional matrix adjust.  
Identities = 197/346 (56%), Positives = 264/346 (76%), Gaps = 3/346 (0%)

Query 18 NGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTV 77  
N T N+T+ +YY H VAA+FI++Y LIF LCM+GNT+VCFIV++N+HMHTV  
Sbjct 122 NDTKHHLYSDINITYVNYLHQPVAAIFIIISYFLIFFLCMMGNTVVCFIVMRNKHMTV 181

Query 78 TNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMSGVLVQGMVSASVFTLVAI 137  
TN+FILNLA+SDLLVGIFCMP TL+DN+I GWPF N CK+SGLVQG+SV+ASVFTLVAI  
Sbjct 182 TNLFILNLAISDLLVGIFCMPITLLDNIIAGWPPGNTMCKISGLVQGISVAASVFTLVAI 241

Query 138 AVERFRICIVHPFREKLTIRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFM-VDARNR 196  
AV+RF+C+V+PF+ KLT++ A V I +IW LA+ IM PSAV L V E+++ + +++N+  
Sbjct 242 AVDRFQCVCVYFPKPKLTIKTAFVIIMIIWLAITIMSPSAVMLHVQEEKYRVRLNSQNK 301

Query 197 SYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVMYARIARKLCQAPGPAPGGEEA 256  
+ P+Y C E WP + MR++YTTVLF++IYLAPL+LIV+MY RI L +A P G +  
Sbjct 302 TSPVYWCREDDWPNQEMRKIYTTVLFANIIYLAPLSLIVIMYGRIGISLFRAAVPHTGRKNQ 361

Query 257 ADPR-ASRRRARVHMLVMVALFFTLSWLPLWALLLLIDYQLSAPQLHLVTVYAFPPAH 315  
SR++ +++ ML++VAL F LSWLPLW L++L DY LS +L ++ +Y +PPAH  
Sbjct 362 EQWHVVSRRKKQIKMLLIALLFILSWLPLWLTMLLSYADLSPNELQIINIYIYPPAH 421

Query 316 WLAFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYS 361  
WLAFF NSS NPIIYG+FNENFRRGFQ AF+ +LC + + EAY+ +  
Sbjct 422 WLAFGNSSVNPIIYGFFNENFRRGFQEAFLQLCQKRAKP-MEAYT 466

>ref|NP\_004876.2| **G** neuropeptide FF receptor 2 isoform 1 [Homo sapiens]  
sp|Q9Y5X5.2|NPFF2\_HUMAN **G** RecName: Full=Neuropeptide FF receptor 2; AltName: Full=Neuropeptide G-protein coupled receptor; AltName: Full=G-protein coupled receptor 74; AltName: Full=G-protein coupled receptor HLWAR77

gb|EAX05649.1| **G** neuropeptide FF receptor 2, isoform CRA\_c [Homo sapiens]  
Length=522

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 420 bits (1080), Expect = 4e-117, Method: Compositional matrix adjust.  
Identities = 197/346 (56%), Positives = 264/346 (76%), Gaps = 3/346 (0%)

```
Query 18 NGTNTTEATPATNLTFSYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHHMTV 77
          N T N+T+ +YY H VAA+FI++Y LIF LCM+GNT+VCFIV++N+HHMTV
Sbjct 122 NDTKHHLYSDNINITYVNYLHQVQVAAIFIISYFLIFFLCMMGNTVVCVIVMRNKHMTV 181

Query 78 TNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMSGLVQGMVSASVFTLVAI 137
          TN+FILNLA+SDLLVGIFCMP TL+DN+I GWPF N CK+SGLVQG+SV+ASVFTLVAI
Sbjct 182 TNLFILNLAISDLLVGIFCMPITLLDNIAGWPFNTMCKISGLVQGISVAASVFTLVAI 241

Query 138 AVERFRFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFM-VDARNR 196
          AV+RF+C+V+PF+ KLT++ A V I +IW LA+ IM PSAV L V E+++ +++++N+
Sbjct 242 AVDRFQCQVVYFPKPKLTIKTAFVIIMIIVLAIITIMSPSAVMLHVQEEKYYRVLNSQNK 301

Query 197 SYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARLCKQAPGAPAGGEEA 256
          + P+Y C E WP + MR++YTTVLF++IYLAPL+LIV+MY RI L +A P G +
Sbjct 302 TSPVYWCREDPWPNQEMRKIYTTVLFANIYLAFLSLIVIMYGRIGISLFRAAVPHTRKKNQ 361

Query 257 ADPR-ASRRRARVHMLVMVALFFTLSWLPLWALLLLIDYQQLSAPQLHLVTYAPPPFAH 315
          SR++ + + + ML++VAL F LSWLPLW L++L DY LS +L ++ +Y +PPFAH
Sbjct 362 EQWHVVSRRKKQKIKMLLIVALLFILSWLPLWTLMLSDYADLSPNELQIINIYIPFAH 421

Query 316 WLAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPSGSHKEAYS 361
          WLAF NSS NPIIYG+FNENFRRGFQ AF+ +LC + + EAY+
Sbjct 422 WLAFGNSSVNPPIYGFNENFRRGFQEAFLQLCQKRAKP-MEAYA 466
```

>gb|EAX05647.1| **G** neuropeptide FF receptor 2, isoform CRA\_a [Homo sapiens]  
Length=304

GENE ID: 10886 NPFFR2 | neuropeptide FF receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 286 bits (732), Expect = 1e-76, Method: Compositional matrix adjust.  
Identities = 135/248 (54%), Positives = 186/248 (75%), Gaps = 3/248 (1%)

```
Query 116 CKMSGLVQGMVSASVFTLVAI AVERFRFCIVHPFREKLTLRKALVTIAVIWALALLIMCP 175
          CK+SGLVQG+SV+ASVFTLVAI AV+RF+C+V+PF+ KLT++ A V I +IW LA+ IM P
Sbjct 2 CKISGLVQGISVAASVFTLVAI AVDRFQCQVVYFPKPKLTIKTAFVIIMIIVLAIITIMSP 61

Query 176 SAVTLTVTREEHHFM-VDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVV 234
          SAV L V E+++ + +++++N+ P+Y C E WP + MR++YTTVLF++IYLAPL+LIV+
Sbjct 62 SAVMLHVQEEKYYRVLNSQNKTS PVYWCREDPWPNQEMRKIYTTVLFANIYLAFLSLIVI 121

Query 235 MYARIARLCKQAPGAPAGGEEAADPRA-SRRRARVHMLVMVALFFTLSWLPLWALLLLI 293
          MY RI L +A P G + SR++ + + + ML++VAL F LSWLPLW L++L
Sbjct 122 MYGRIGISLFRAAVPHTRKKNQEQWHVVSRRKKQKIKMLLIVALLFILSWLPLWTLMLLS 181

Query 294 DYQQLSAPQLHLVTYAPPPFAH WLAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPS 353
          DY LS +L ++ +Y +PPFAH WLAF NSS NPIIYG+FNENFRRGFQ AF+ +LC +
Sbjct 182 DYADLSPNELQIINIYIPFAH WLAFGNSSVNPPIYGFNENFRRGFQEAFLQLCQK-R 240

Query 354 GSHKEAYS 361
          EAY+
Sbjct 241 AKPMEAYA 248
```

>ref|NP\_001517.2| **G** orexin receptor 2 [Homo sapiens]

sp|O43614.2|OX2R\_HUMAN **G** RecName: Full=Orexin receptor type 2; AltName: Full=Ox2r; AltName: Full=Hypocretin receptor type 2

emb|CAH73407.1| **G** hypocretin (orexin) receptor 2 [Homo sapiens]

emb|CAI19665.1| **G** hypocretin (orexin) receptor 2 [Homo sapiens]

gb|EAX04440.1| **G** hypocretin (orexin) receptor 2 [Homo sapiens]  
Length=444

GENE ID: 3062 HCRT2 | hypocretin (orexin) receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 190 bits (483), Expect = 7e-48, Method: Compositional matrix adjust.  
Identities = 128/376 (34%), Positives = 189/376 (50%), Gaps = 41/376 (10%)

```
Query 6 SQPPNSSWPLSQNGTNTTEA-----TPATNLTFSY----YQHTSPVAAMFIVAYALIFLL 56
          PP +W + T+ T + F Y Y H + I Y ++F++
Sbjct 8 DSPPCNRNWSASELNBTQEPFLNPTDYDDEEFLRYLWREYLPKEYEVL IAGYIIVFV 67

Query 57 CMVGNTLVCFIVLKNRHHMTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATC 116
          ++GN LVC V KN HM TVTN FI+NL+++D+LV I C+P TLV ++ W F + C
Sbjct 68 ALIGNVLVCVAVWKNHHMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLC 127

Query 117 KMSGLVQGMVSASVFTLVAI AVERFRFCIVHPFREKLTLRKALVTIAVIWALALLIMCPS 176
          K+ +Q+SVS SV TL IA++R+ I HP K T ++A +I +IW ++ +IM P
Sbjct 128 KVIPYIQLTQTSVSVSVTLTSCIALDRWYAICHPLMPKSTAKRARNISIVIWIWVSCIIMIPQ 187

Query 177 AVTLTVTREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMY 236
          A+ + E N++ C E W + ++Y F Y+AFL L+V+ Y
Sbjct 188 AIVM---ECSTVFPLANKTTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAY 243

Query 237 ARIARL-C-QAPGPA-----PG-----GEEAADPRASRRRARVV 269
          +I RKL C Q PG + PG AA+ + R R +
Sbjct 244 LQIFRKLWCRQIPGTSSVVQRKWKLPQVSPRPGQPTKSRMSAVAABIKQIRARRKTA 303
```



Query 270 HMLVMVALFFTLISWLPWALLLLIDYQGLSAPQLHLVTVYA-PPFAHWLAFFNSSANPII 328  
 ML++V L F + +LP+ L +L + A TVYA F F+HWL + NS+ANPII  
 Sbjct 304 RMLMIVLLVFAICYLPISILNVLKRVFGMFAHTEDETVYAWFTFSHWLVYANSAANPII 363

Query 329 YGYFNENFRRGFQAAF 344  
 Y + + FR F+AAF  
 Sbjct 364 YNFLSGKFREEFKAAF 379

>gb|AAC39602.1| **G** orexin receptor-2; OX2R; G protein-coupled receptor [Homo sapiens]  
 gb|AAG28021.1| **G** hypocretin receptor-2 [Homo sapiens]  
 gb|AAL47215.1| **G** hypocretin receptor 2; orexin receptor 2 [Homo sapiens]  
 dbj|BAG36939.1| **G** unnamed protein product [Homo sapiens]  
 Length=444

GENE ID: 3062 HCRTR2 | hypocretin (orexin) receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 190 bits (483), Expect = 7e-48, Method: Compositional matrix adjust.  
 Identities = 128/376 (34%), Positives = 189/376 (50%), Gaps = 41/376 (10%)

Query 6 SQPPNSSWPLSQNGTNTTEA-----TPATNLTFSY---YQHTSPVAAMFIVAYALIFLL 56  
 PP +W + T+ T + F Y Y H + I Y ++F++  
 Sbjct 8 DSPPCRNWSSASELNETQEPFLNPTDYDDEEFLRYLWREYLPKEYEYEWLIAGYIIVFVV 67

Query 57 CMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATC 116  
 ++GN LVC V KN HM TVTN FI+NL+++D+LV I C+P TLV ++ W F + C  
 Sbjct 68 ALIGNVLVCVAVWKNHMRVTNIFYIVNLSLADVLVTITCLPATLVVDITETWFFGQSLC 127

Query 117 KMSGLVQMGMSVASVFTLVIAIAVERFRFCIVHPFREKLTLRKALVTIAVIWALALLIMCPS 176  
 K+ +Q +SVS SV TL IA++R+ I HP K T ++A +I +IW ++ +IM P  
 Sbjct 128 KVIPLYLQTVSVSVSVTLTSCIALDRWYAICHPLMPKSTAKRARNISIVIIWIVSCIIMIPQ 187

Query 177 AVTLTVTREHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMY 236  
 A+ + E N++ C E W + ++Y F Y+APL L+V+ Y  
 Sbjct 188 AIVM---ECSTVFPGLANKTTTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAY 243

Query 237 ARIARKL-C-QAPGPA-----PG-----GEEAADPRASRRRARVV 269  
 +I RKL C Q PG + PG AA+ + R R +  
 Sbjct 244 LQIFRKLWCRIQIPSTSSVVQRKWKPLQPVSQPRGPGQPTKSRMSAVAAETKQIRARRKTA 303

Query 270 HMLVMVALFFTLISWLPWALLLLIDYQGLSAPQLHLVTVYA-PPFAHWLAFFNSSANPII 328  
 ML++V L F + +LP+ L +L + A TVYA F F+HWL + NS+ANPII  
 Sbjct 304 RMLMIVLLVFAICYLPISILNVLKRVFGMFAHTEDETVYAWFTFSHWLVYANSAANPII 363

Query 329 YGYFNENFRRGFQAAF 344  
 Y + + FR F+AAF  
 Sbjct 364 YNFLSGKFREEFKAAF 379

>gb|AAC39601.1| **G** orexin receptor-1; OX1R; G protein-coupled receptor [Homo sapiens]  
 Length=425

GENE ID: 3061 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 181 bits (459), Expect = 4e-45, Method: Compositional matrix adjust.  
 Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMS 119  
 GNTLVC V +N HM TVTN FI+NL+++D+LV C+P +L+ ++ W F +A CK+  
 Sbjct 63 GNTLVCLAVRNHMRVTNIFYIVNLSLADVLVTAICLPASLVDITESWLFGHALCKVI 122

Query 120 GLVQMGMSVASVFTLVIAIAVERFRFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVT 179  
 +Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A  
 Sbjct 123 PYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQAAV 182

Query 180 LTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARI 239  
 + E + + NR+ C E W + ++Y + F YLAPL L+ + Y +I  
 Sbjct 183 M----ECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQI 238

Query 240 ARKLC--QAPG-----PAPGGEE--AADPRASRRRARVVH 270  
 RKL Q PG P P G A+ + R R +  
 Sbjct 239 FRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAK 298

Query 271 MLVMVALFFTLISWLPWALLLLIDYQGLSAPQLHLVTVYA-PPFAHWLAFFNSSANPIIY 329  
 ML++V L F L +LP+ L +L + VYA F F+HWL + NS+ANPIIY  
 Sbjct 299 MLMVVLVLFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIY 358

Query 330 GYFNENFRRGFQAAFRARL-----CPRPSGSHKE 358  
 + + FR F+AAF L PR S SHK  
 Sbjct 359 NPLSGKFRQFKAAFSCCLPGLGPCGSLKAPSPRSSASHKS 399

>ref|NP\_001516.2| **G** orexin receptor 1 [Homo sapiens]  
 sp|O43613.2|OX1R\_HUMAN **G** RecName: Full=Orexin receptor type 1; AltName: Full=Hypocretin receptor type 1  
 gb|AAG28020.1| **G** hypocretin receptor-1 [Homo sapiens]  
 gb|AAL47214.1| **G** hypocretin receptor 1; orexin receptor 1 [Homo sapiens]  
 gb|AAL50221.1| **G** hypocretin receptor 1 [Homo sapiens]  
 gb|AAH74796.1| **G** Hypocretin (orexin) receptor 1 [Homo sapiens]  
 gb|EAX07602.1| **G** hypocretin (orexin) receptor 1, isoform CRA\_c [Homo sapiens]  
 Length=425

GENE ID: 3061 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 179 bits (453), Expect = 2e-44, Method: Compositional matrix adjust.  
 Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMS 119

```

Sbjct 63 GNTLVLC V +N HM TVTN FI+NL+++D+LV C+P +L+ ++ W F +A CK+ 122
GNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFPGHALCKVI

Query 120 GLVQGMVSASVFTLVVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVT 179
+Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A
Sbjct 123 PYLQAVSVSAVLTLSFIALDRWYAICHPLLPKSTARRARGSILGIWAVSLAIMVPQAAV 182


Query 180 LTVTREEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARI 239
+ E + + NR+ C E W + ++Y + F YLAPL L+ + Y +I
Sbjct 183 M----ECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQI 238

Query 240 ARKLC--QAPGPAPG-----GEEAAD-----PRAS-----RRRARVVH 270
RKL Q PG ++ D PRA R R +
Sbjct 239 FRKLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLEAVKQMRARRKTAK 298

Query 271 MLVMVALFFTLWSLPLWALLLLIDYQLSAPQLHLVTVYA-FPFAHWLAFFNSSANPIIY 329
ML++V L F L +LP+ L +L + VYA F F+HWL + NS+ANPIIY
Sbjct 299 MLMVVLLVLFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIY 358

Query 330 GYFNENFRRGFQAAFRARL-----CPRPSGSHKE 358
+ + FR F+AAF L PR S SHK
Sbjct 359 NFLSGKFRQFKAAAFSCCLPGLGPCGSLKAPSPRSSASHKS 399

```

>dbj|BAF83210.1|  unnamed protein product [Homo sapiens]  
Length=425

GENE ID: 3061 HCRTR1 | hypocretin (orexin) receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 179 bits (453), Expect = 2e-44, Method: Compositional matrix adjust.  
Identities = 122/341 (35%), Positives = 171/341 (50%), Gaps = 46/341 (13%)

```

Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMS 119
GNTLVLC V +N HM TVTN FI+NL+++D+LV C+P +L+ ++ W F +A CK+
Sbjct 63 GNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFPGHALCKVI 122

Query 120 GLVQGMVSASVFTLVVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVT 179
+Q +SVS +V TL IA++R+ I HP K T R+A +I IWA++L IM P A
Sbjct 123 PYLQAVSVSAVLTLSFIALDRWYAICHPLLPKSTARRARGSILGIWAVSLAIMVPQAAV 182


Query 180 LTVTREEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARI 239
+ E + + NR+ C E W + ++Y + F YLAPL L+ + Y +I
Sbjct 183 M----ECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQI 238


Query 240 ARKLC--QAPGPAPG-----GEEAAD-----PRAS-----RRRARVVH 270
RKL Q PG ++ D PRA R R +
Sbjct 239 FRKLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLEAVKQMRARRKTAK 298









Query 271 MLVMVALFFTLWSLPLWALLLLIDYQLSAPQLHLVTVYA-FPFAHWLAFFNSSANPIIY 329
ML++V L F L +LP+ L +L + VYA F F+HWL + NS+ANPIIY
Sbjct 299 MLMVVLLVLFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIY 358

Query 330 GYFNENFRRGFQAAFRARL-----CPRPSGSHKE 358
+ + FR F+AAF L PR S SHK
Sbjct 359 NFLSGKFRQFKAAAFSCCLPGLGPCGSLKAPSPRSSASHKS 399

```

>ref|NP\_000901.1|  neuropeptide Y receptor Y2 [Homo sapiens]

sp|P49146.1|NPY2R\_HUMAN  RecName: Full=Neuropeptide Y receptor type 2; Short=NPY2-R; AltName:  
Full=NPY-Y2 receptor; Short=Y2 receptor

gb|AAC50281.1|  neuropeptide Y/peptide YY Y2 receptor  
gb|AAB04120.1|  neuropeptide y2 receptor  
gb|AAC51115.1|  type 2 neuropeptide Y receptor  
gb|AAO92062.1|  neuropeptide Y receptor Y2 [Homo sapiens]  
gb|AAH75052.2|  Neuropeptide Y receptor Y2 [Homo sapiens]  
gb|AAH75053.2|  Neuropeptide Y receptor Y2 [Homo sapiens]  
gb|AAY40940.1|  unknown [Homo sapiens]  
gb|EAX04901.1|  neuropeptide Y receptor Y2 [Homo sapiens]  
Length=381

GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 167 bits (422), Expect = 9e-41, Method: Compositional matrix adjust.  
Identities = 112/322 (34%), Positives = 164/322 (50%), Gaps = 23/322 (7%)

```

Query 42 VAAMPFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101
V + I+AY I LL ++GN+LV +V+K + M TVTN FI NLAV+DLLV C+P TL
Sbjct 49 VQVLLILAYCSIIILGVIGNSLVHVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTL 108

Query 102 VDNLTITGWPFNDATCKMSGLVQGMVSASVFTLVVAIAVERFCIVHPFREKLTLRKALVT 161
L+ W C + QG++V S TL IA++R RCIV+ K++ R + +
Sbjct 109 TYTLMGEWKMGFVLCVLPYAQGLAVQVSTITLTIVIALDRHRCIVYHLESKISKISPLI 168

Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCEAWP--EKGMRRVYTT 218
I + W ++ L+ P L + RE + + + C E W P EK + VY+
Sbjct 169 IGLAWGISALLASP---LAIFREYSLIEIIP---DFEIVACTEKWPGEEKSIYGTVYSL 221

Query 219 VLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALF 278
+Y+ PL +I Y RI KL P AA+ +RR + MLV V +
Sbjct 222 SSSLILYVLPGLIISFSYTRIWSKLKNHVSFG-----AANDHYHQRQKTTKMLVCVVVV 276

Query 279 FTLWSLPLWALLLLIDYQ--LSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYFNENF 336
F +SWLPL A L +D L + L+ F H +A ++ ANP++YG+ N N+
Sbjct 277 FAVSWLPLHAFQLAVDIDSQVLDLKEYKLI----FTVFHIIAMCSTFANPLLYGWMNSNY 332

Query 337 RRGFOAAFRARLCPRPSGSHKE 358
R+ F +AFR R H E
Sbjct 333 RKAFLSAFRCE--QRLDAIHSE 352

```

>gb|AAA93170.1| **G** type 2 neuropeptide Y receptor  
Length=381

GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 165 bits (417), Expect = 3e-40, Method: Compositional matrix adjust.  
Identities = 111/322 (34%), Positives = 163/322 (50%), Gaps = 23/322 (7%)

```
Query 42  VAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101
          V + I+AY I LL ++GN+LV +V+K + M TVTN FI NLAV+DLLV C+P TL
Sbjct 49  VQVVLILAYCSIILLGVIGNSLVIHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTL 108

Query 102  VDNLITGWPFNDATCKMSGLVQMSVSASVFTLVIAIAVERFCIVHPFREKLTLRKALVT 161
          L+ W C + QG++ S TL IA++R RCIV+ K++ R + +
Sbjct 109  TYTLMGEWKMGPVLCHLVPAQGLAAQVSTITLTIVIALDRHRCIVYHLESKISKRISFLI 168

Query 162  IAVIWALALIMCPSAVTLTVTREEHHFMVDARNRSYPLYSWEAWP--EKGMR-RVYTT 218
          I + W ++ L+ P L + RE + + + C E WP EK + VY+
Sbjct 169  IGLAWGISALLASP----LAIFREYSLIEIIP---DFEIVACTEKWPGEEKSIYGTVYSL 221

Query 219  VLFShIYLAPLALIVVMYARIARKLCQAPGPAPGEEAADPRASRRRRARVVHMLVMVALF 278
          +Y+ PL +I Y RI KL P AA+ +RR + MLV V +
Sbjct 222  SSLLILYVLPGLIISFSYTRIWSKLKNHVS PG-----AANDHYHQRRQKTTKMLVCVVVV 276

Query 279  FTLSWLPLWALLLLIDYQG--LSAPQLHLVTVYAFPAHWAFFNSSANPIIYGYNENF 336
          F +SWLPL A L +D L + L+ F H +A ++ ANP++YG+ N N+
Sbjct 277  FAVSWLPLHAFQLAVDIDSQVLDLKEYKLI---FTVFHIIAMCSTFANPLLYGWMNSNY 332

Query 337  RRGFQAAPRARLCPRPSGSHKE 358
          R+ F +APR R H E
Sbjct 333  RKAFLSAFRCE--QRLDAIHSE 352
```

>ref|NP\_937822.2| **G** G protein-coupled receptor 103 [Homo sapiens]

sp|Q96P65.2|QRFP\_HUMAN **G** RecName: Full=Orexigenic neuropeptide QRFP receptor; AltName: Full=G-protein coupled receptor 103; AltName: Full=SP9155;  
AltName: Full=AQ27

gb|EAX05262.1| **G** G protein-coupled receptor 103, isoform CRA\_b [Homo sapiens]  
Length=431

GENE ID: 84109 QRFP | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer PubMed links)

Score = 165 bits (417), Expect = 3e-40, Method: Compositional matrix adjust.  
Identities = 93/304 (30%), Positives = 159/304 (52%), Gaps = 21/304 (6%)

```
Query 51  ALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWP 110
          LIF L + GN LV ++V +++ M TVTN+FI +LA+SDLL+ FC+P T++ N+ W
Sbjct 53  VLIFALALFGNALVFYVVTNRKAMRTVTNIFICSLALSDDLITFCIPVTMLQNISDNWL 112

Query 111  FDNATCKMSGLVQMSVSASVFTLVIAIAVERFCIVHPFREK--LTLRKALVTIAVIWAL 168
          CKM VQ +V + T+ I AVER + +VHPP+ K T R+A + V+W +
Sbjct 113  GGAFICKMVVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMKQYTNRRFTMLGVVWL 172

Query 169  ALLIMCP--SAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKGMRRVYTTVLFShIYL 226
          A+++ P L + ++ F+ + + C E W +++YTT + ++L
Sbjct 173  AVIVGSPMWHVQQLEI---KYDFLYEKEH-----ICCLEEWTSFVHQKIYTTFILVILFL 224

Query 227  APLALIVVMYARIARKLCQAPGPAPG-----GEEAADPRASRRRRARVVHMLVMVALFF 279
          PL +++++Y++I +L G G+E + + +R++ R V M+V V F
Sbjct 225  LPLMVMLILYSKIGYELWIKKRVGDGSLRTIHGKEMS--KIARKKKRAVIMMVTVVALF 282

Query 280  TLSWLPLWALLLLIDYQLSAPQLHLVTVYAFPAHWAFFNSSANPIIYGYNENFRRG 339
          + W P + ++I+Y + F + F NS NPI+Y + NENF++
Sbjct 283  AVCWAPFHVHMMIEYSNFEKEYDDVTIKMIFAIVQIIGFSNSICNPIVAFMNENFKKN 342

Query 340  FQAA 343
          +A
Sbjct 343  VLSA 346
```

>dbj|BAC98938.1| **G** QRFP receptor [Homo sapiens]  
Length=431

GENE ID: 84109 QRFP | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer PubMed links)

Score = 164 bits (416), Expect = 4e-40, Method: Compositional matrix adjust.  
Identities = 93/304 (30%), Positives = 159/304 (52%), Gaps = 21/304 (6%)

```
Query 51  ALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWP 110
          LIF L + GN LV ++V +++ M TVTN+FI +LA+SDLL+ FC+P T++ N+ W
Sbjct 53  VLIFALALFGNALVFYVVTNRKAMRTVTNIFICSLALSDDLITFCIPVTMLQNISDNWL 112


Query 111  FDNATCKMSGLVQMSVSASVFTLVIAIAVERFCIVHPFREK--LTLRKALVTIAVIWAL 168
          CKM VQ +V + T+ I AVER + +VHPP+ K T R+A + V+W +
Sbjct 113  GGAFICKMVVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMKQYTNRRFTMLGVVWL 172

Query 169  ALLIMCP--SAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKGMRRVYTTVLFShIYL 226
          A+++ P L + ++ F+ + + C E W +++YTT + ++L
Sbjct 173  AVIVGSPMWHVQQLEI---KYDFLYEKEH-----ICCLEEWTSFVHQKIYTTFILVILFL 224

Query 227  APLALIVVMYARIARKLCQAPGPAPG-----GEEAADPRASRRRRARVVHMLVMVALFF 279
          PL +++++Y++I +L G G+E + + +R++ R V M+V V F
Sbjct 225  LPLMVMLILYSKIGYELWIKKRVGDGSLRTIHGKEMS--KIARKKKRAVIMMVTVVALF 282

Query 280  TLSWLPLWALLLLIDYQLSAPQLHLVTVYAFPAHWAFFNSSANPIIYGYNENFRRG 339
          + W P + ++I+Y + F + F NS NPI+Y + NENF++
Sbjct 283  AVCWAPFHVHMMIEYSNFEKEYDDVTIKMIFAIVQIIGFSNSICNPIVAFMNENFKKN 342

Query 340  FQAA 343
          +A
Sbjct 343  VLSA 346
```

>gb|AAD00248.1|  neuropeptide Y receptor type 2 [Homo sapiens]  
Length=381

GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 164 bits (416), Expect = 5e-40, Method: Compositional matrix adjust.  
Identities = 111/322 (34%), Positives = 164/322 (50%), Gaps = 23/322 (7%)

```
Query 42  VAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101
          V + I+AY I LL ++GN+LV +V+K + M TVTN FI NLAV+DLLV C+P TL
Sbjct 49  VQVVLILAYCSIIILGVIGNSLVHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTL 108


Query 102 VDNLITGWPFDNATCKMSGVLVQGMSVSASVFTLVIAIAVERFCRIVHPFREKLTLRKALVT 161
          L+ W C + OG++V S TL IA++R RCIV+ K++ R + +
Sbjct 109 TYTLMGEWKMGPVLCHLVFPAQGLAVQVSTITLTIVIALDRHRCIVYHLESKISKRISFLI 168

Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCWEAWP--EKGMR-RVYTT 218
          I + W ++ L+ P L + RE + + + C E WP EK + VY+
Sbjct 169 IGLAWGISALLASP----LAIFREYSLIEIIP---DFEIVACTEKWPGEESKIYGTVYSL 221

Query 219 VLFShIYLAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALF 278
          +Y+ PL +I Y RI KL P AA+ +RR + MLV V +
Sbjct 222 SSSLILLYLPLGIISFSYTRIWSKLKSHVSPG-----AANDHYHQRRQKTKMLVCVVVV 276

Query 279 FTLSWLPWLWALLLLIDYQG--LSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENF 336
          F +SWLPL A L +D L + L+ F + +A ++ ANP++YG+ N N+
Sbjct 277 FAVSWLPPLHAFQLAVDIDSQVLDLKEYKLI----FTVFYIIAMCSTFANPLLYGWMNSNY 332

Query 337 RRGFQAAPFRARLCPRPSGSHKE 358
          R+ F +AFR R H E
Sbjct 333 RKAPLSAFRCE--QRLDAIHSE 352
```

>gb|AAB07760.1|  neuropeptide y/peptide YY receptor type 2  
Length=381

GENE ID: 4887 NPY2R | neuropeptide Y receptor Y2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 164 bits (414), Expect = 6e-40, Method: Compositional matrix adjust.  
Identities = 112/322 (34%), Positives = 163/322 (50%), Gaps = 23/322 (7%)

```
Query 42  VAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101
          V + I+AY I LL ++GN+LV +V+K + M TVTN FI NLAV+DLLV C+P TL
Sbjct 49  VQVVLILAYCSIIILGVIGNSLVHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTL 108


Query 102 VDNLITGWPFDNATCKMSGVLVQGMSVSASVFTLVIAIAVERFCRIVHPFREKLTLRKALVT 161
          L+ W C + OG++V S TL IA++R RCIV+ K++ R + +
Sbjct 109 TYTLMGEWKMGPVLCHLVFPAQGLAVQVSTITLTIVIALDRHRCIVYHLESKISKRISFLI 168

Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCWEAWP--EKGMR-RVYTT 218
          I + W ++ L+ P L + RE + + + C E WP EK + VY+
Sbjct 169 IGLWGISALLASP----LAIFREYSLIEIIP---DFEIVPCTEKWPAAEKSIYGTVYSL 221

Query 219 VLFShIYLAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALF 278
          +Y+ PL +I Y RI KL P AA+ +RR + MLV V +
Sbjct 222 SSSLILLYLPLGIISFSYTRIWSKLKSHVSPG-----AANDHYHQRRQKTKMLVCVVVV 276

Query 279 FTLSWLPWLWALLLLIDYQG--LSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENF 336
          F +SWLPL A L +D L + L+ F + +A ++ ANP++YG+ N N+
Sbjct 277 FAVSWLPPLHAFQLAVDIDSQVLDLKEYKLI----FTVFHIIAMCSTFANPLLYGWMNSNY 332

Query 337 RRGFQAAPFRARLCPRPSGSHKE 358
          R+ F +AFR R H E
Sbjct 333 RKAPLSAFRCE--QRLDAIHSE 352
```

>gb|AAA59920.1|  neuropeptide y receptor  
Length=384

GENE ID: 4886 NPY1R | neuropeptide Y receptor Y1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 160 bits (405), Expect = 8e-39, Method: Compositional matrix adjust.  
Identities = 106/316 (33%), Positives = 162/316 (51%), Gaps = 17/316 (5%)

```
Query 41  PVAAMFIVA--YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMP 98
          P+A +F +A Y + +L + GN + I+LK + M VTN+ I+NL+ SDLLV I C+P
Sbjct 36  PLAMIFTLALAYGAVIILGVSGNLALIIILKQKEMRNVTNIIIVNLVSFSDLLVAIMCLP 95


Query 99  TTLVDNLITGWPFDNATCKMSGVLVQGMSVSASVFTLVIAIAVERFCRIVHPFREKLTLRKA 158
          T V L+ W F A CK++ VQ +S++ S+F+LV IAVR+ I++P + R A
Sbjct 96  LTFVYITLMDHWVFGAMCKLNPFVQCVSITVSIFSLVLIIVERHQLIINPRGWRPNNRHA 155


Query 159 LVTIAVIWALALLIMCPSAVTLTVTREE--HHFMDARNRSYPLYSCWEAWPEKGMRRVYT 217
          V IAVIW LA+ P + +T E + +DA Y C++ +P R YT
Sbjct 156 YVGIAVIWLVAVASSLPFLIYQVMTDEPFQNVTLDAYKDKYV--CFDQFPSDSHRLSYT 212


Query 218 TLFShIYLAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVAL 277
          T+L Y PL I + Y +I +L + + + +R + ML+ + +
Sbjct 213 TLLLVQLQYFGPLCFIFICYFKIYIRLKRNNMMDKMRDNKYSSETKRNINI--MLLSIVV 270

Query 278 FFTLSWLPWLWALLLLIDYG--QLSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENF 336
          F + WLPL + D+ Q+ A H + F H A ++ NPI YG+ N+NF
Sbjct 271 AFAVCWLPLTIFNTVFDWNHQIATCNHNL---LFLLCHLTAMISTCVNPIFYGFLNKNF 327

Query 337 RRGFQ-----AAFRAR 347
          +R Q FR+R
Sbjct 328 QRDQLQFFNFCDFRSR 343
```


>ref|NP\_000900.1|  neuropeptide Y receptor Y1 [Homo sapiens]

sp|P25929.1|NPY1R HUMAN  RecName: Full=Neuropeptide Y receptor type 1; AltName: Full=NPY1-R


gb|AAA73215.1|  [Human neuropeptide Y peptide YY receptor mRNA, complete cds.],  
gene product




8 more sequence titles

gb|AAA59947.1|  neuropeptide Y receptor Y1  
gb|AAH36657.1|  Neuropeptide Y receptor Y1 [Homo sapiens]  
gb|AAS55647.1|  neuropeptide Y1 receptor [Homo sapiens]  
gb|AAH71720.1|  Neuropeptide Y receptor Y1 [Homo sapiens]  
gb|EAX04841.1|  neuropeptide Y receptor Y1 [Homo sapiens]  
dbj|BAG35472.1|  unnamed protein product [Homo sapiens]  
Length=384  
GENE ID: 4886 NPY1R | neuropeptide Y receptor Y1 [Homo sapiens]  
(Over 10 PubMed links)  
Score = 160 bits (404), Expect = 1e-38, Method: Compositional matrix adjust.  
Identities = 106/316 (33%), Positives = 162/316 (51%), Gaps = 17/316 (5%)  
Query 41 PVAAMFIVA--YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMP 98  
P+A +F +A Y + +L + GN + I+LK + M VTN+ I+NL+ SLLV I C+P  
Sbjct 36 PLAMITPLALAYGAVIILGVSGNLALIIILKQKEMRNVTNLIIVNLSFSDLLVAIMCLP 95  
Query 99 TTLVDNLITGWFPDNATCKMSGLVQGMVSASVFTLVIAIAVERFCRIVHPFREKLTLRKA 158  
T V L+ W F A CK++ VQ +S++ S+F+LV IAVR + I++P + R A  
Sbjct 96 FTFVYTLMDHWVPEAMCKLNPVQCVSITVSIFSLVLIIVERHQLIINPRGWRPNRHA 155  
Query 159 LVTIAVIWALALLIMCPSAVTLTVTREE-HHFMVDARNRSYPLYSWEAWPEKMRVYT 217  
V IAVI W LA+ P + +T E + +DA Y C++ +P R YT  
Sbjct 156 YVGIAVIWVLAVASSLPFLIYQVMTDEPFQNVTLDAYKDKYV---CFDQFSDSHRLSYT 212  
Query 218 TVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGGEEAADPRASRRRARVHMLVMVAL 277  
T+L Y PL I + Y +I +L + + +R + ML+ + +  
Sbjct 213 TLLLVLYQYGPLCFIFICYFKIYIRLKRNNMMDKMRDNKYRSSETKRINI--MLLSIVV 270  
Query 278 FFTLSWLPLWALLLLIDYG-QLSAPQLHLVTYVAFPAHWLAFFNSSANPIIYGYNENF 336  
F + WLPL + D+ Q+ A H + F H A ++ NPI YG+ N+NF  
Sbjct 271 AFAVCWLPFLTIFNTVFDWNHQIATCNHNL--LFLCHLTAMISTCVNPIFYGLNKNF 327  
Query 337 RRGFQ-----AAFRAR 347  
+R Q FR+R  
Sbjct 328 QRDLPFFNFCDFRSR 343

>gb|AAF43705.1|AF236081\_1  orphan G-protein coupled receptor GPR72 [Homo sapiens]  
Length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
(10 or fewer PubMed links)  
Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
Identities = 105/322 (32%), Positives = 166/322 (51%), Gaps = 22/322 (6%)  
Query 42 VAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101  
V A+ IVAY+ I + + GN LVC ++ KN+ MH+ T++FI+NLAV+D+++ + P TL  
Sbjct 70 VKALLIVAYSFIIVFSLFGNVLVCHVIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTL 129  
Query 102 VDNLTITGWFPDNATCKMSGLVQGMVSASVFTLVIAIAVERFCRIVHPFREKLTLRKALVT 161  
V + + W F C +S Q S+ S TL AIAV+R + I+HP + +++ K ++  
Sbjct 130 VRFVNSTWIFGKGMCHVSRFAQYCSLHVSALTTLTAIAVDRHQVIMHPLKPRISITKGVYI 189  
Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKG---MRRVYTTV 219  
IAVIW +A P A+ + ++ + RS C +PE +  
Sbjct 190 IAVIWTMATFFSLPHAICQKLFYFKYS---EDIVRSL---CLPDFPEPADLFWKYLDLA 242  
Query 220 LFSHIYLAFLALIVVMYARIARK--LCQAPGAPGGEEAADPRASRRRARVHMLVMVAL 277  
F +Y+ PL +I V YAR+A+K LC G + A R++ + + ML++V +  
Sbjct 243 TFILLYLPLLIISVAYARVAKKLWLCNMIGDVTTEQYFA---LRRKKKTIKMLMLVVV 299  
Query 278 FFTLSWLPLWALLLLIDYGQLSAPQLHLVTYVAFPAHWLAFFNSSANPIIYGYNENFR 337  
F L W PL +LL LS+ + F F HW A ++ NP IY + NENFR  
Sbjct 300 LFPALCWFPPLNCYVLL----LSSKVIRTNALYFAP-HWFAMSSTCYNPFYICWLNENFR 353  
Query 338 RGFQAARFARLCPRPSGSHKEA 359  
+A +C RP ++  
Sbjct 354 IELKALL--SMCQRPPKQEDG 373

>sp|Q9NYM4.2|GPR83\_HUMAN  RecName: Full=Probable G-protein coupled receptor 83; AltName:  
Full=G-protein coupled receptor 72; Flags: Precursor

gb|AAH67473.1|  G protein-coupled receptor 83 [Homo sapiens]  
gb|EAW66929.1|  G protein-coupled receptor 83 [Homo sapiens]  
dbj|BAG37605.1|  unnamed protein product [Homo sapiens]  
Length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
(10 or fewer PubMed links)  
Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)  
Query 42 VAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101  
V A+ IVAY+ I + + GN LVC ++ KN+ MH+ T++FI+NLAV+D+++ + P TL  
Sbjct 70 VKALLIVAYSFIIVFSLFGNVLVCHVIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTL 129  
Query 102 VDNLTITGWFPDNATCKMSGLVQGMVSASVFTLVIAIAVERFCRIVHPFREKLTLRKALVT 161  
V + + W F C +S Q S+ S TL AIAV+R + I+HP + +++ K ++  
Sbjct 130 VRFVNSTWIFGKGMCHVSRFAQYCSLHVSALTTLTAIAVDRHQVIMHPLKPRISITKGVYI 189  
Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKG---MRRVYTTV 219  
IAVIW +A P A+ + ++ + RS C +PE +  
Sbjct 190 IAVIWTMATFFSLPHAICQKLFYFKYS---EDIVRSL---CLPDFPEPADLFWKYLDLA 242  
Query 220 LFSHIYLAFLALIVVMYARIARK--LCQAPGAPGGEEAADPRASRRRARVHMLVMVAL 277  
F +Y+ PL +I V YAR+A+K LC G + A R++ + + ML++V +

Sbjct 243 TFILLYILPLLIISVAYARVAKKLWLCNMIGDVTTEQYFA---LRRKKKTIKMLMLVVV 299

Query 278 FFTLSWLPLWALLLLIDYQQLSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFR 337  
 F L W PL +LL LS+ + F F HW A ++ NP IY + NENFR

Sbjct 300 LFALCWFPNLCYVLL----LSSKVIRTNALYFAP-HWFAMSSTCYNPFIYCWLNNENFR 353

Query 338 RGFQAAPFRARLCPRPSGSHKE 358  
 +A +C RP ++

Sbjct 354 IELKALL--SMCQRPPKPQED 372

>ref|NP\_057624.2| **UG** G protein-coupled receptor 83 [Homo sapiens]  
 gb|ABY87919.1| **G** G protein-coupled receptor 83 [Homo sapiens]  
 Length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLLCMVGNLTLCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101  
 V A+ IVAY+ I + + GN LVC ++ KN+ MH+ T++FI+NLAV+D+++ + P TL

Sbjct 70 VKALLIVAYSFIIVFSLFGNVLVCHVIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTL 129

Query 102 VDNLTITGWFPDNATCKMSGLVQGMVSASVFTLVAVIAVERFRCIVHPFREKLTLRKALVT 161  
 V + + W F C +S Q S+ S TL AIAV+R + I+HP + +++ K ++

Sbjct 130 VRFVNSTWIFGKGMCHVSRFAQYCSLHVSALTTLTAIAVDRHQVIMHPLKPRISITKGVY 189

Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKG--MRRVYTTV 219  
 IAVIW +A P A+ + ++ + RS C +PE +

Sbjct 190 IAVIWTMATFFSLPHATCQKLFTFKYS---EDIVRSL---CLPDFPEPADLFWKYLDLA 242

Query 220 LFSHIYLAPLALIVVMYARIARK--LCQAPGPAPGGEAAADPRASRRRARVHMLVMVAL 277  
 F +Y+ PL +I V YAR+A+K LC G + A R++ + + ML++V +

Sbjct 243 TFILLYILPLLIISVAYARVAKKLWLCNMIGDVTTEQYFA---LRRKKKTIKMLMLVVV 299

Query 278 FFTLSWLPLWALLLLIDYQQLSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFR 337  
 F L W PL +LL LS+ + F F HW A ++ NP IY + NENFR

Sbjct 300 LFALCWFPNLCYVLL----LSSKVIRTNALYFAP-HWFAMSSTCYNPFIYCWLNNENFR 353

Query 338 RGFQAAPFRARLCPRPSGSHKE 358  
 +A +C RP ++

Sbjct 354 IELKALL--SMCQRPPKPQED 372

>dbj|BAA96064.1| **G** KIAA1540 protein [Homo sapiens]  
 Length=424

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 156 bits (395), Expect = 1e-37, Method: Compositional matrix adjust.  
 Identities = 105/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLLCMVGNLTLCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101  
 V A+ IVAY+ I + + GN LVC ++ KN+ MH+ T++FI+NLAV+D+++ + P TL

Sbjct 71 VKALLIVAYSFIIVFSLFGNVLVCHVIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTL 130

Query 102 VDNLTITGWFPDNATCKMSGLVQGMVSASVFTLVAVIAVERFRCIVHPFREKLTLRKALVT 161  
 V + + W F C +S Q S+ S TL AIAV+R + I+HP + +++ K ++

Sbjct 131 VRFVNSTWIFGKGMCHVSRFAQYCSLHVSALTTLTAIAVDRHQVIMHPLKPRISITKGVY 190

Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKG--MRRVYTTV 219  
 IAVIW +A P A+ + ++ + RS C +PE +

Sbjct 191 IAVIWTMATFFSLPHATCQKLFTFKYS---EDIVRSL---CLPDFPEPADLFWKYLDLA 243

Query 220 LFSHIYLAPLALIVVMYARIARK--LCQAPGPAPGGEAAADPRASRRRARVHMLVMVAL 277  
 F +Y+ PL +I V YAR+A+K LC G + A R++ + + ML++V +

Sbjct 244 TFILLYILPLLIISVAYARVAKKLWLCNMIGDVTTEQYFA---LRRKKKTIKMLMLVVV 300

Query 278 FFTLSWLPLWALLLLIDYQQLSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFR 337  
 F L W PL +LL LS+ + F F HW A ++ NP IY + NENFR

Sbjct 301 LFALCWFPNLCYVLL----LSSKVIRTNALYFAP-HWFAMSSTCYNPFIYCWLNNENFR 354

Query 338 RGFQAAPFRARLCPRPSGSHKE 358  
 +A +C RP ++

Sbjct 355 IELKALL--SMCQRPPKPQED 373

>gb|AAH67474.1| **G** G protein-coupled receptor 83 [Homo sapiens]  
 Length=423

GENE ID: 10888 GPR83 | G protein-coupled receptor 83 [Homo sapiens]  
 (10 or fewer PubMed links)

Score = 152 bits (385), Expect = 2e-36, Method: Compositional matrix adjust.  
 Identities = 103/321 (32%), Positives = 166/321 (51%), Gaps = 22/321 (6%)

Query 42 VAAMFIVAYALIFLLCMVGNLTLCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTL 101  
 V A+ IVAY+ I + + GN LVC ++ KN+ +H+ T++FI+NLAV+++++ + P TL

Sbjct 70 VKALLIVAYSFIIVFSLFGNVLVCHVIFKNQRVHSATSLFIVNLAVANIMITLLNTPFTL 129

Query 102 VDNLTITGWFPDNATCKMSGLVQGMVSASVFTLVAVIAVERFRCIVHPFREKLTLRKALVT 161  
 V + + W F C +S Q S+ S TL AIAV+R + I+HP + +++ K ++

Sbjct 130 VRFVNSTWIFGKGMCHVSRFAQYCSLHVSALTTLTAIAVDRHQVIMHPLKPRISITKGVY 189

Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKG--MRRVYTTV 219  
 IAVIW +A P A+ + ++ + RS C +PE +


Sbjct 190 IAVIWTMATFFSLPHATCQKLFTFKYS---EDIVRSL---CLPDFPEPADLFWKYLDLA 242

Query 220 LFSHIYLAPLALIVVMYARIARK--LCQAPGPAPGGEAAADPRASRRRARVHMLVMVAL 277  
 F +Y+ PL +I V YAR+A+K LC G + A R++ + + ML++V +

Sbjct 243 TFILLYILPLLIISVAYARVAKKLWLCNMIGDVTTEQYFA---LRRKKKTIKMLMLVVV 299

Query 278 FFTLSWLPLWALLLLIDYQQLSAPQLHLVTVYAFPPFAHWAFFNSSANPIIYGYNENFR 337  
 F L W PL +LL LS+ + F F HW A ++ NP IY + NENFR





Sbjct 300 LFLALCWFLNLCYVLL----LSSKVIRTNALYFAF-HWFAMSSTCYNPFIYCWLNNENFR 353  
Query 338 RGFQAAFRARLCPRPSGSHKE 358  
+A +C RP ++  
Sbjct 354 IELKALL--SMCQRPPKPQED 372











>gb|AAI28134.1|  GPR103 protein [Homo sapiens]  
Length=356

GENE ID: 84109 QRFPFR | pyroglutamylated RFamide peptide receptor [Homo sapiens]  
(10 or fewer PubMed links)

Score = 149 bits (375), Expect = 2e-35, Method: Compositional matrix adjust.  
Identities = 84/281 (29%), Positives = 144/281 (51%), Gaps = 21/281 (7%)

Query 74 MHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPPDNATCKMSGLVQGMVSASVFT 133  
M TVTN+FI +IA+SDLL+ FC+P T++ N+ W CKM VQ +V + T  
Sbjct 1 MRTVTNFIICSLALSDLLITFFCIPVTMLQNISDNWLGGAFCIKMVPFVQSTAVVTEILT 60  
Query 134 LVAIAVERFRCIVHPFREK--LTLRKALVTIAVIWALLIMCP--SAVTLTVTREEHHF 189  
+ IAVER + +VHPF+ K T R+A + V+W +A+++ P L + ++ F  
Sbjct 61 MTCIAVERHQGLVHPFKMKWQYTNRRAPTMLGVVWLVAIVGSPMWHVQQLLEI---KYDF 117  
Query 190 MVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGP 249  
+ + + C E W +++YTT + ++L PL +++++Y++I +L  
Sbjct 118 LYEKEH-----ICCLEEWTSPVHQKIYTTFILVLFLPLMLVMLILYSKIGYELWIKKRV 172  
Query 250 APG-----GEEAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYGQLSAPQ 302  
G G+E + +R++ R V M+V V F + W P + ++I+Y  
Sbjct 173 GDGSVLRTIHGKEMS--KIARKKKRAVIMMVTVVALFAVCWAPFHVHMMIEYSNFEKEY 230  
Query 303 LHLVTVYAPPPFAHWLAFFNSSANPIIYGYPNENFRRGFQAA 343  
+ F + F NS NPI+Y + NENF++ +A  
Sbjct 231 DDVTIKMIFAIVQIIGFSNSICNPVYAFMNENFKKNVSSA 271

>ref|NP\_003848.1|   galanin receptor 2 [Homo sapiens]  
sp|O43603.1|GALR2\_HUMAN  RecName: Full=Galanin receptor type 2; AltName: Full=GAL2-R;  
AltName: Full=GALR2  
gb|AAC39634.1|  galanin receptor GalR2 [Homo sapiens]  
10 more sequence titles

gb|AAC18118.1|  galanin receptor subtype 2 [Homo sapiens]  
gb|AAC36587.1|  galanin receptor type 2 [Homo sapiens]  
gb|AAD08671.1|  galanin receptor type 2 [Homo sapiens]  
gb|AAH69130.1|  Galanin receptor 2 [Homo sapiens]  
gb|AAH74914.1|  Galanin receptor 2 [Homo sapiens]  
gb|AAH74915.1|  Galanin receptor 2 [Homo sapiens]  
gb|AAI09053.1|  Galanin receptor 2 [Homo sapiens]  
gb|AAI09052.1|  Galanin receptor 2 [Homo sapiens]  
gb|EAW89364.1|  galanin receptor 2 [Homo sapiens]  
gb|ABQ52421.1|  galanin receptor 2 [Homo sapiens]  
Length=387

GENE ID: 8811 GALR2 | galanin receptor 2 [Homo sapiens] (Over 10 PubMed links)

Score = 148 bits (374), Expect = 3e-35, Method: Compositional matrix adjust.  
Identities = 122/373 (32%), Positives = 181/373 (48%), Gaps = 42/373 (11%)

Query 41 PVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTT 100  
P A + +ALIFL+ VGNTLV ++L+ + TN+FILNL V+DL + C+P  
Sbjct 23 PEAVIVPLLLFALIFLVGTVGNTLVLAVALLRGGQAVSTTNLFILNLGVADLCFILCCVPFQ 82  
Query 101 LVDNLITGWPPDNATCKMSGLVQGMVSASVFTLVAIAVERFRCIVHPF--REKLTLRKA 158  
+ GW F + CK + +++ AS FTL A++++R+ I +P RE T R A  
Sbjct 83 ATIYTLDGWVFGSLLCXAVHFLIFLTMHASSFTLAASVSLDRYLAIIRYPLHSRELRTPRNA 142  
Query 159 LVTTIAVIWALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTT 218  
L I +IW L+LL P L+ R+ ++ L C AW RR  
Sbjct 143 LAAIGLIWGLSLLFSGP---YLSYYRQ-----SQLANLTVCHPAWSAP-RRRAMDI 189  
Query 219 VLFSHIYLAFLALIVVMYARIARKLCQAPGPAPGGEAADPRASRRRARVVHMLVMVALF 278  
F YL P+ ++ + YAR R L +A P AA A R + +V M+++VA  
Sbjct 190 CTFVFSYLLPVVLVLGLTYARTLRYLWRAVDPV----AAGSGARRAKRKVTRMILIVAAL 244  
Query 279 FTLSWLPWLWALLLLIDYGQLSAPQLHLVTVYAFP-FAHWLAFFNSSANPIIYGYPNENFR 337  
F L W+P AL+L + +GQ + YA +H +++ NS NPI+Y +++FR  
Sbjct 245 FCLCWMPPHAILICVWFGQPPLTR---ATYALRILSHLVSYANSCVNPVYALVSKHFR 300  
Query 338 RGF-----QAAFRA--RLCPRPSGSHKEAYSERPGG-LLH-RRVFWVVRPSDSGLP 384  
+GF +A RA R+C G+H + ER LLH +RP P  
Sbjct 301 KGFRTICAGLLGRAPGRASGRVCAAARGTHSGSVLERESSDLLHMSEAAGALRPC----P 356  
Query 385 SESGPSSGAPRPG 397  
S P P PG  
Sbjct 357 GASQPCILEPCPG 369

>gb|AAB05897.1|  neurokinin-2 receptor  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 148 bits (373), Expect = 4e-35, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 185/408 (45%), Gaps = 25/408 (6%)

Query 21 NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNM 80  
N + P +N T ++ + S A++ AY + L+ + GN +V +I+L +R M TVTN

Sbjct	11	NISSGPESNTTGTTFAPSPMSWQLALWATAYLALVLVAVTGNAIIVIWIILAHRRMRTVTNY	70
Query	81	FILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMSGLVQGMSSVSASVFTLVIAIAVE	140
Sbjct	71	FI+NLA++DL + F V W F A C L ++ S++++ AIA +	
Sbjct	71	FIVNLALADLCMAAFNAFNFVYASHNIWYFGRAPCYFQNLFPITAMFVSIYSMTAIAAD	130
Query	141	RFRCTIVHPPREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPL	200
Sbjct	131	R+ IVHPP+ +L+ IA IW +AL + P TVT ++	
Sbjct	131	RYMAIVHPPQPLRSAPSTKAVIAGIWLVALALASPQCFYSTVTMDQ-----GA	178
Query	201	YSCWEAWPEKGMRR--VYTTVLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEAA-	256
Sbjct	179	C AWPE + +Y V+ + IY PLA++ V Y+ I L + P G +A	
Sbjct	179	TKCVVWAPEDSGGKTLTLLYHLVVIALIYFLPLAVMFVAYSIGLTLWRRRAVP---GHQAH	235
Query	257	-ADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYQQLSAPQLHLVTVYAFPPFAH	315
Sbjct	236	A+ R + + + V +V+V L F + WLP +L + + + VY F	
Sbjct	236	GANLRHLQAKKFKVKTMLVVLTPAICWLPYHLYFILGSFQEDIYCHKFIQQVYLALF--	293
Query	316	WLAFNNSANPIIYGYFNENFRRGFQAAFRARLCPRPSGSHKEAYSERPGGLLHRRVFVV	375
Sbjct	294	WLA ++ NPIIY N FR GF+ AFR CP + + ++ P L RV	
Sbjct	294	WLAMSTMYNPPIIYCCLNHRFRSGFRLAFRC--CPWVTPTKEDKLELTPTTSLSTRVNRC	351
Query	376	VRPSDGLPSESGPSSGAPRPRGRLPLRNGRVAHHGLPREGPGCSHLPL	423
Sbjct	352	+ ++ PS P +G G P +H+ +	
Sbjct	352	HTKETLFMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTCTHVEI	398

>gb|AAH99637.1| **G** Pancreatic polypeptide receptor 1 [Homo sapiens]  
Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 148 bits (373), Expect = 4e-35, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 166/336 (49%), Gaps = 19/336 (5%)

Query	14	PLSQNGTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRH	73
Sbjct	12	P S G N T FS + Q + V + +Y++ ++ ++GN + + + +	
Sbjct	12	PKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKE	71
Query	74	MHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMSGLVQGMSSVSASVFT	133
Sbjct	72	VTN+ I NLA SD L+ + C P T V ++ W F CKMS +Q MSV+ S+ +	
Sbjct	72	KANVTNLLIANLAFSDFLMCLLCQPLTAVTYTMDYWIFGETLCKMSAFIQCMSVTVSILS	131
Query	134	LVAIAVERFRFCIVHPPREKLTLRKALVTIAVIWALALLIMCP---SAVTLTVTREEH---	187
Sbjct	132	LV +A+ER + I++P K ++ +A + I +IW +A ++ P +++ V + H	
Sbjct	132	LVLVALERHQILINPTGWKPSISQAYLGIVLIWVIACVLSLPLANSILENVFHKNSKA	191
Query	188	-HFMVDARNRSYPLYSWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARKLCQA	246
Sbjct	192	F+ D C E+WP R +YTT L Y PL I+V YARI R+L Q	
Sbjct	192	LEFLADK-----VVCESWPLAHHRTIYTTFLLLFQYCLPLGFILVCYARIYRRL-QR	243
Query	247	PGPAPGGEAAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYQQLSAPQLHLV	306
Sbjct	244	G + ++ VV ++++VA F + WLPL L D+ + P H	
Sbjct	244	QGRVFHKGYSRLRAGHMKQVNVVLVVMVA--FAMLWLPLHVFNSLEDWHHEAIPICHGN	301
Query	307	TVYAFPPFAHWLAFNNSANPIIYGYFNENFRRGFQA	342
Sbjct	302	+ F H LA ++ NP IYG+ N NF++ +A	
Sbjct	302	LI--FLVCHLLAMASTCVNPFYIGFLNTNFKKEIKA	335

>ref|NP\_000721.1| **UG** cholecystokinin A receptor [Homo sapiens]

sp|P32238.1|CKKAR HUMAN **G** RecName: Full=Cholecystokinin receptor type A; AltName: Full=CCK-A receptor; Short=CCK-AR; AltName: Full=Cholecystokinin-1 receptor; Short=CCK1-R

gb|AAA35659.1| **G** cholecystokinin A receptor  
7 more sequence titles

gb|AAA02819.1| **G** cholecystokinin A receptor  
gb|AAA91123.1| **G** cholecystokinin type A receptor  
dbj|BAA90879.1| **G** cholecystokinin type-A receptor [Homo sapiens]  
gb|AAP84362.1| **G** cholecystokinin A receptor [Homo sapiens]  
gb|AAH74987.1| **G** Cholecystokinin A receptor [Homo sapiens]  
gb|EAW92850.1| **G** cholecystokinin A receptor [Homo sapiens]  
dbj|BAG36692.1| **G** unnamed protein product [Homo sapiens]  
Length=428

GENE ID: 886 CCKAR | cholecystokinin A receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 147 bits (370), Expect = 8e-35, Method: Compositional matrix adjust.  
Identities = 109/353 (30%), Positives = 173/353 (49%), Gaps = 61/353 (17%)

Query	44	AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD	103
Sbjct	42	A+ I+ Y+LIFLL ++GNTLV ++++N+ M TVTN+F+L+LAVSDL++ +FCMP L+	
Sbjct	42	AVQILLYSLIFLLSVLGNLTIVTLIRNKRMTVTNIFLLSLAVSDLMCLFCMPFNLI	101
Query	104	NLITGWPFDNATCKMSGLVQGMSSVSASVFTLVIAIAVERFRFCIVHPPREKL--TLRKALVT	161
Sbjct	102	NL+ + F +A CK + G SVS S F LVAI++ER+ I P + ++ T AL	
Sbjct	102	NLLKDFIFGSVAVCTTTFYFMGTSVSVSTFNLVAISLERYGAICKPLQSRVWQTKSHALKV	161
Query	162	IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKGMRRVYTTVL	221
Sbjct	162	IA W L+ IM P + + + +N + C P M++ + T L	
Sbjct	162	IAATWCLSFRTIMTPYPI-----YSNLVPFTKNNQNTANMCRFLLPNDVMQSWHTFL	214
Query	222	SHIYLAPLALIVVMYARIARKLCQA-----PGPAPGGE-EAAD-----	258
Sbjct	215	++L P ++++V Y I+ +L Q P G+ E +D	
Sbjct	215	LILFLIPGIVMMVAYGLISLELYQGIKFEASQKSAKERKPTSTSSGKYEDSDGCYLQKT	274
Query	259	-----PRASRRRA-----RVVHMLVMVALFFTLWSLPLWALL	291
Sbjct	275	RA+R R+ RV+ ML+++ F L W+P+++	
Sbjct	275	RPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIRMLIVVLFFLCWMPIFSANA	334



Query 292 LIDYGQLSAPQLHLVTYVAFPPFAHWAFFNSSANPIIYGYFNENFRRGFQAAF 344  
Y SA ++ F L++ +S NPIIY + N+ FR GF A F  
Sbjct 335 WRAYDTASAER--RLSGTPISFILLLSYTSSCVNPIIYCFMKNRFRLGFMATF 385

>sp|P21452.2|NK2R\_HUMAN [G] RecName: Full=Substance-K receptor; Short=SKR; AltName: Full=Neurokinin A receptor; AltName: Full=NK-2 receptor; Short=NK-2R;  
AltName: Full=Tachykinin receptor 2  
gb|AAB20303.1| neurokinin-2 receptor, NK-2 receptor [human, Peptide, 398 aa]  
gb|AAP84358.1| [G] tachykinin receptor 2 [Homo sapiens]  
gb|EAW54324.1| [G] tachykinin receptor 2, isoform CRA\_a [Homo sapiens]  
dbj|BAF84685.1| [G] unnamed protein product [Homo sapiens]  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 146 bits (369), Expect = 1e-34, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 184/408 (45%), Gaps = 25/408 (6%)

Query 21 NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNM 80  
N + P + N T + + S A++ AY + L+ + GN +V +I+L +R M TVTN  
Sbjct 11 NISSGPESNTTGITAFSMPSWQLALWATAYLALVLVAVTGNAIWIILAHRRMRTVTNY 70  
Query 81 FILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMSGLVQGMVSASVFTLVIAIAVE 140  
FI+NLA++DL + F V W F A C L ++ S+++ AIA +  
Sbjct 71 FIVNLALADLCMAAFNAAFNFVYASHNIWYFGRFCYFQNLFPITAMFVSIYSMTAIAAD 130  
Query 141 RFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPL 200  
R+ IVHPP+ +L+ IA IW +AL + P TVT ++  
Sbjct 131 RYMAIVHPPQRLSAPSTKAVIAGIWLVALALASPCFYSTVTMDQ-----GA 178  
Query 201 YSCWEAWPEKGMRR--VYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGGEAA- 256  
C AWPE + +Y V+ + IY PLA++ V Y+ I L + P G +A  
Sbjct 179 TKCVVWAPEDSGGKTLILYHLVVIALLIYFLPLAVMFVAYSIGLTLWRRVAVP---GHQAH 235  
Query 257 -ADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLIDYGQLSAPQLHLVTYVAFPPFAH 315  
A+ R + + + V +V+V L F + WLP +L + + + VY F  
Sbjct 236 GANLRHLQAKKKFVKTMVLVLTFAICWLPYHLYFILGSFQEDIYCHKFIQQVYLALF-- 293  
Query 316 WLAFFNSSANPIIYGYFNENFRRGFQAAFRARLCPRPSGSHKEAYSERPGGLLHRRVFVV 375  
WLA ++ NPIIY N FR GF+ AFR CP + + ++ P L RV  
Sbjct 294 WLAMSSTMYNPIIYCLNHRFRSGFRLAFRC--CPWVTPTKEDKLELTPTTSLSTRVNRC 351  
Query 376 VRPSDGLPSESGPSSGAPRGRPLRNGRVAHHGLPREGPGCSHLPL 423  
+ ++ PS P ++G G P +H+ +  
Sbjct 352 HTKETLFMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTCTHVEI 398

>gb|AAC31760.1| [G] neurokinin A receptor [Homo sapiens]  
gb|AAA60347.1| [G] neurokinin A receptor  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 184/408 (45%), Gaps = 25/408 (6%)

Query 21 NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNM 80  
N + P + N T + + S A++ AY + L+ + GN +V +I+L +R M TVTN  
Sbjct 11 NISSGPESNTTGITAFSMPSWQLALWAPYALALVLVAVTGNAIWIILAHRRMRTVTNY 70  
Query 81 FILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMSGLVQGMVSASVFTLVIAIAVE 140  
FI+NLA++DL + F V W F A C L ++ S+++ AIA +  
Sbjct 71 FIVNLALADLCMAAFNAAFNFVYASHNIWYFGRFCYFQNLFPITAMFVSIYSMTAIAAD 130  
Query 141 RFRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPL 200  
R+ IVHPP+ +L+ IA IW +AL + P TVT ++  
Sbjct 131 RYMAIVHPPQRLSAPSTKAVIAGIWLVALALASPCFYSTVTMDQ-----GA 178  
Query 201 YSCWEAWPEKGMRR--VYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGGEAA- 256  
C AWPE + +Y V+ + IY PLA++ V Y+ I L + P G +A  
Sbjct 179 TKCVVWAPEDSGGKTLILYHLVVIALLIYFLPLAVMFVAYSIGLTLWRRVAVP---GHQAH 235  
Query 257 -ADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLIDYGQLSAPQLHLVTYVAFPPFAH 315  
A+ R + + + V +V+V L F + WLP +L + + + VY F  
Sbjct 236 GANLRHLQAKKKFVKTMVLVLTFAICWLPYHLYFILGSFQEDIYCHKFIQQVYLALF-- 293  
Query 316 WLAFFNSSANPIIYGYFNENFRRGFQAAFRARLCPRPSGSHKEAYSERPGGLLHRRVFVV 375  
WLA ++ NPIIY N FR GF+ AFR CP + + ++ P L RV  
Sbjct 294 WLAMSSTMYNPIIYCLNHRFRSGFRLAFRC--CPWVTPTKEDKLELTPTTSLSTRVNRC 351  
Query 376 VRPSDGLPSESGPSSGAPRGRPLRNGRVAHHGLPREGPGCSHLPL 423  
+ ++ PS P ++G G P +H+ +  
Sbjct 352 HTKETLFMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTCTHVEI 398

>ref|NP\_005963.3| [G] pancreatic polypeptide receptor 1 [Homo sapiens]

sp|P50391.1|NPY4R\_HUMAN [G] RecName: Full=Neuropeptide Y receptor type 4; Short=NPY4-R; AltName: Full=Pancreatic polypeptide receptor 1; Short=PP1  
gb|AAC50280.1| [G] neuropeptide Y4 receptor protein  
emb|CAA91433.1| [G] pancreatic polypeptide receptor PP1 [Homo sapiens]  
gb|AAP23199.1| [G] pancreatic polypeptide receptor 1 [Homo sapiens]  
emb|CAI13318.1| [G] pancreatic polypeptide receptor 1 [Homo sapiens]  
gb|AAV68197.1| [G] pancreatic polypeptide receptor 1 [Homo sapiens]  
Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 167/336 (49%), Gaps = 19/336 (5%)

```
Query 14 PLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRH 73
          P S G N T FS + Q + V + +Y++ ++ ++GN + + ++ +
Sbjct 12 PKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKE 71



Query 74 MHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSGVQMSVSASVFT 133
          VTN+ I NLA SD L+ + C P T V ++ W F CKMS +Q MSV+ S+ +
Sbjct 72 KANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILS 131

Query 134 LVAIAVERFCRIVHPFREKLTLRKALVTIAVIWALALLIMCP---SAVTLTVTREEH--- 187
          LV +A+ER + I++P K ++ +A + I +IW +A ++ P +++ V + H
Sbjct 132 LVLVALERHQILIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKHNSKA 191

Query 188 -HFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIARKLCQA 246
          F+ D C E+WP R +YTT L Y PL I+V YARI R+L +
Sbjct 192 LEFLADK-----VVCTESWPLAHHRTIYTTFLLLFYQCLPLGFILVCYARIYRRLQRO 244

Query 247 PGPAPEGEEAADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLIDYGQLSAPQLHLV 306
          G + RA + +V +LV++ + F + WLPL L D+ + P H
Sbjct 245 GRVFKHGTYSL--RAGHMK-QVNVVLVVMVAVFAVLWPLHVFNSLEDWHHEAIPICHGN 301

Query 307 TVYAFPPFAHWLAFNSSANPIIYGYFNENFRRGFOA 342
          + F H LA ++ NP IYG+ N NF++ +A
Sbjct 302 LI--FLVCHLLAMASTCVNPFYIGFLNTNFKKEIKA 335
```

>ref|NP\_001048.2|  tachykinin receptor 2 [Homo sapiens]  
dbj|BAC05952.1|  seven transmembrane helix receptor [Homo sapiens]  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 145 bits (366), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 117/408 (28%), Positives = 183/408 (44%), Gaps = 25/408 (6%)

```
Query 21 NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHMTVTNM 80
          N + P +N T + + S A++ AY + L+ + GN +V +I+L +R M TVTN
Sbjct 11 NISSGPESENTTGIATFASMPWSQLALWATAYLALVLVAVTGNAIWIILAHRRMRTVTNY 70

Query 81 FILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSGVQMSVSASVFTLVAIAVE 140
          FI+NLA++DL + F V W F A C L ++ S++++ AIA +
Sbjct 71 FIVNLALADLCMAAFNAAFNFVYASHNIWYFGRAPCYFQNLFPITAMFVSIYSMTAIAAD 130




Query 141 RFRCLIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPL 200
          R+ IVHPF+ +L+ IA IW +AL + P TVT ++
Sbjct 131 RYMAIVHPFPRLSAPSTKAVIAGIWLVALALASPCFYSTVTMDQ-----GA 178

Query 201 YSCWEAWPEKGMRR---VYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGPAPEGEEA- 256
          C AWPE + +Y V+ + IY PLA++ V Y+ I L + P G +A
Sbjct 179 TKCVVWVEDSGGKTLTLLYHLVIALIYFLPLAVMFVAVSVIGLTLWRRRAVP---GHQAH 235

Query 257 -ADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLIDYGQLSAPQLHLVTVYAFPPFAH 315
          A+ R + + V +V+V L F + WLP +L + + + VY F
Sbjct 236 GANLRHLQAMKKFVKTMVLVVLTFALICWLPYHLYFYFLGFSQEDIYCHKFIQQVYLALF-- 293

Query 316 WLAFNSSANPIIYGYFNENFRRGFOAARLARLCPRPSGSHKEAYSERPGGLLHRRVFVV 375
          WLA ++ NPIIY N PR GF+ AFR CP + + ++ P L RV
Sbjct 294 WLAMSSMYNPIIYCCLNHRFRSGFRLAFRC--CPWVTPTEKDEKLELTPTTSLSTRVNRC 351

Query 376 VRPSDGLSPSESGAPRPGRLPLRNGRVAHHGLPREGPGCSHLPL 423
          + ++ PS P ++G G P +H+ +
Sbjct 352 HTKETLFMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTCTHVEI 398
```

>gb|AAB07759.1|  pancreatic polypeptide receptor  
gb|AAV68196.1|  pancreatic polypeptide receptor 1 [Homo sapiens]  
gb|AAH96238.1|  Pancreatic polypeptide receptor 1 [Homo sapiens]  
Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 145 bits (365), Expect = 3e-34, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 167/336 (49%), Gaps = 19/336 (5%)

```
Query 14 PLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRH 73
          P S G N T FS + Q + V + +Y++ ++ ++GN + + ++ +
Sbjct 12 PKSPQGENRSKPLGTPYNFSEHCQDSVDVMVFIVTSYSIETVVGVLGNLCLMCVTVRQKE 71

Query 74 MHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSGVQMSVSASVFT 133
          VTN+ I NLA SD L+ + C P T V ++ W F CKMS +Q MSV+ S+ +
Sbjct 72 KANVTNLLIANLAFSDFLMCLLCQPLTSVYTIMDYWIFGETLCKMSAFIQCMSVTVSILS 131

Query 134 LVAIAVERFCRIVHPFREKLTLRKALVTIAVIWALALLIMCP---SAVTLTVTREEH--- 187
          LV +A+ER + I++P K ++ +A + I +IW +A ++ P +++ V + H
Sbjct 132 LVLVALERHQILIINPTGWKPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHKHNSKA 191

Query 188 -HFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIARKLCQA 246
          F+ D C E+WP R +YTT L Y PL I+V YARI R+L +
Sbjct 192 LEFLADK-----VVCTESWPLAHHRTIYTTFLLLFYQCLPLGFILVCYARIYRRLQRO 244

Query 247 PGPAPEGEEAADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLIDYGQLSAPQLHLV 306
          G + RA + +V +LV++ + F + WLPL L D+ + P H
Sbjct 245 GRVFKHGTYSL--RAGHMK-QVNVVLVVMVAVFAVLWPLHVFNSLEDWHHEAIPICHGN 301

Query 307 TVYAFPPFAHWLAFNSSANPIIYGYFNENFRRGFOA 342
          + F H LA ++ NP IYG+ N NF++ +A
Sbjct 302 LI--FLVCHLLAMASTCVNPFYIGFLNTNFKKEIKA 335
```

>emb|CAG46748.1|  PPYR1 [Homo sapiens]  
Length=375

GENE ID: 5540 PPYR1 | pancreatic polypeptide receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 143 bits (361), Expect = 9e-34, Method: Compositional matrix adjust.  
Identities = 103/336 (30%), Positives = 166/336 (49%), Gaps = 19/336 (5%)

Query	14	PLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRH	73
		P S G N T F S + Q + V + +Y++ ++ ++GN + + + + +	
Sbjct	12	PKSPQGENRSKPLGTPYNFSEHCQDSVDMVFIVTSYSIETVVGVLGNLCLMCVTVRQKE	71
Query	74	MHTVTNMFILNLAVALDVLGVFCMPTTLVDNLITGWPFDPNATCKMSGVQGMVSASVFT	133
		VTN+ I NLA SD L+ + C P T V ++ W F CKMS +Q MSV+ S+ +	
Sbjct	72	KANVTNLLIANLAFSDFLMCLLCQPLTAVYTIMDYWIFGETLCKMSAFIQCMSVTVSILS	131
Query	134	LVAIAVERFRFCIVHPFREKLTLRKALVTIAVIWALALLIMCP---SAVTLTVTREEH---	187
		LV +A+ER + I++P K ++ +A + I +IW +A ++ P +++ V + H	
Sbjct	132	LVLVALERHQLIINPTGWKPSISQAYLGIWIVACVLSLPLANSILENVFHKHNSKA	191
Query	188	-HFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARKLCQA	246
		F + D C E+WP R +YTT L Y PL I+V YARI R L +	
Sbjct	192	LEFLADK-----VVCESWPLAHHRTIYTTFLLLFQYCLPLGFLVLCYARIYRCLQRQ	244
Query	247	PGPAPGGEAAADPRASRRRARVHMLVMVALFFTLWLPLWALLLLIDYQLSAPQLHLV	306
		G + RA + +V +LV++ + F + WLPL L D+ + P H	
Sbjct	245	GRVFHKGTYSL--RAGHMK-QVNVVLVVMVFAVLWLPLHVFNSLEDWHHEAIPICHGN	301
Query	307	TVYAFPPFAHWAFFNSSANPIIYGYNENFRRGFQA	342
		+ F H LA ++ NP IYG+ N NF++ +A	
Sbjct	302	LI--FLVCHLLAMASTCVNPFYIGFLNTNFKKEIKA	335

>gb|EAW54325.1| **G** tachykinin receptor 2, isoform CRA\_b [Homo sapiens]  
Length=399

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 142 bits (357), Expect = 3e-33, Method: Compositional matrix adjust.  
Identities = 117/409 (28%), Positives = 184/409 (44%), Gaps = 26/409 (6%)

Query	21	NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNM	80
		N + P +N T + + S A++ AY + L+ + GN +V +I+L +R M TVTN	
Sbjct	11	NISSGPESNTTGTAFSMPSWQLALWATAYLALVLVAVTGNAIIVIIAHRRMRVTNY	70
Query	81	FILNLAVALDVLGVFCMPTTLVDNLITGWPFDPNATCKMSGVQGMVSASVFTLVIAIVE	140
		FI+NLA++DL + F V W F A C L ++ S++++ AIA +	
Sbjct	71	FIVNLALADLCMAAFNAFNVYASHNIWYFGRAFQYFQNLFPITAMFVSIYSMTAIAAD	130
Query	141	R-FRCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYP	199
		R + IVHPP+ +L+ IA IW +AL + P TVT ++	
Sbjct	131	RQYMAIVHPQPRLSAPSTKAVIAGIWLVALALASPQCIFYSTVTMDQ-----G	178
Query	200	LYSCWEAWPEKGMRR---VYTTVLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEAA	256
		C AWPE + +Y V+ + IY PLA++ V Y+ I L + P G +A	
Sbjct	179	ATKCVVAVPEDSGKTLTLLYHLVVIALLYFLPLAVMFVAYSIGLTLWRRAPV---GHQA	235
Query	257	--ADPRASRRRARVHMLVMVALFFTLWLPLWALLLLIDYQLSAPQLHLVTVYAFPPFA	314
		A + R + + + + V +V+V L F + WLP +L + + + VY F	
Sbjct	236	HGANLRHLQAKKKFVKTMVLVLTFAICWLPYHLYFIFLGSFQEDIYCHKFIQQVYLALF-	294
Query	315	HWLAFFNSSANPIIYGYNENFRRGFQAARARLCPRPSGSHKEAYSERPGGLLHRRVVFV	374
		WLA ++ NPIIY N FR GF+ AFR CP + + ++ P L RV	
Sbjct	295	-WLAMSTMYNPIIYCCNLHRFRSGFRLAFRC--CPWVTPTKEDKLELTPTTSLSTRVNR	351
Query	375	VVRPSDGLPSESGPAPRPGRLPLRNGRVAHHGLPREGPGCSHLPL	423
		+ ++ PS P +G G P +H+ +	
Sbjct	352	CHTKETLFMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTKTHVEI	399

>gb|AAH96842.1| **G** Tachykinin receptor 2 [Homo sapiens]  
Length=398

GENE ID: 6865 TACR2 | tachykinin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 140 bits (353), Expect = 9e-33, Method: Compositional matrix adjust.  
Identities = 115/408 (28%), Positives = 182/408 (44%), Gaps = 25/408 (6%)

Query	21	NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNM	80
		N + P +N T + + S A++ AY + L+ + GN +V +I+L +R M TVTN	
Sbjct	11	NISSGPESNTTGTAFSMPSWQLALWATAYLALVLVAVTGNAIIVIIAHRRMRVTNY	70
Query	81	FILNLAVALDVLGVFCMPTTLVDNLITGWPFDPNATCKMSGVQGMVSASVFTLVIAIVE	140
		FI+NLA++DL + F V W F A C L ++ S++++ AIA +	
Sbjct	71	FIVNLALADLCMAAFNAFNVYASHNIWYFGRAFQYFQNLFPITAMFVSIYSMTAIAAD	130
Query	141	RFRICIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPL	200
		R+ IVHPP+ +L+ IA IW +AL + P TVT ++	
Sbjct	131	RYMAIVHPPQPRLSAPSTKAVIAGIWLVALALASPQCIFYSTVTMDQ-----GA	178
Query	201	YSCWEAWPEKGMRR---VYTTVLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEAA	256
		C AWPE + +Y V+ + IY PLA++ V Y+ I L + P G +A	
Sbjct	179	TKCVVAVPEDSGKTLTLLYHLVVIALLYFLPLAVMFVAYSIGLTLWRRAPV---GHQA	235
Query	257	-ADPRASRRRARVHMLVMVALFFTLWLPLWALLLLIDYQLSAPQLHLVTVYAFPPFAH	315
		A+ R + + + + V +V+V L F + W P +L + + + VY F	
Sbjct	236	GANLRHLQAKKKFVKTMVLVLTFAICWPPYHLYFIFLGSFQEDIYCHKFIQQVYLALF--	293
Query	316	WLAFNSSANPIIYGYNENFRRGFQAARARLCPRPSGSHKEAYSERPGGLLHRRVVFV	375
		WLA ++ NPIIY N FR GF+ AFR CP + + ++ L RV	
Sbjct	294	WLAMSTMYNPIIYCCNLHRFRSGFRLAFRC--CPWVTPTKEDKLELTPTTSLSTRVNR	351
Query	376	VVRPSDGLPSESGPAPRPGRLPLRNGRVAHHGLPREGPGCSHLPL	423
		+ ++ PS P +G G P +H+ +	
Sbjct	352	HTKETLFMAGDTAPSEATSGEAGRP-QDGSGLWFGYGLLAPTKTHVEI	398

>gb|AAB20304.1| substance K receptor, SK receptor [human, Peptide, 398 aa]  
Length=398

Score = 139 bits (350), Expect = 2e-32, Method: Compositional matrix adjust.  
Identities = 116/402 (28%), Positives = 181/402 (45%), Gaps = 36/402 (8%)

```
Query 21 NTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNM 80
          N + P +N T + + S A++ A + L+ + GN +V +I+L +R M TVTN
Sbjct 11 NISSGPESNTTGTITAFSPMSQWLALWATAVLALVLVAVTGNAIWIILAHRRMRTVTNY 70

Query 81 FILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSGLVQGMVSASVFTLVIAIVE 140
          FI+NLA++DL + F V W F A C L ++ S++++ AIA +
Sbjct 71 FIVNLALADLCMAAFNAAFNFVYASHNIWYFGRACFYQNLFPITAMFVSIYSMTAIAAD 130

Query 141 RFRICVHHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPL 200
          R+ IVHPP+ +L+ IA IW +AL + P TVT ++
Sbjct 131 RYMAIVHPPQRLSAPSTKAVIAGIWLVALALASPQCFYSTVTMDQ-----GA 178

Query 201 YSCWEAWPEKGMRR--VYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGPGGEEA- 256
          C AWPE +Y V+ + IY PLA++ V Y+ I L + P G +A
Sbjct 179 TKCVVWAPEDSGGKTLLEYHLVVIALLYFLPLAVMFVAVSVIGLTLWRRRAVP--GHQAH 235

Query 257 -ADPRASRRRRARVHMLVMVALFFTLISWLPWALLLLIDYQLSAPQLHLVTYAPFFAH 315
          A+ R + + + V +V+V L F + WLP +L + + + VY F
Sbjct 236 GANLRHLQAKKKFVKTMVLVLTFAICWLPYHLYFILGSPQEDIYCHKFIQVYLALF-- 293

Query 316 WLAFNNSANPIIYGYNENFRRGFQAARLCPRPSGSHKEYAYERPGGLLHRRVFFV 375
          WLA + + NPITY N FR GF+ AFR CP + + + P L RV
Sbjct 294 WLAMSSTMYNPPIIYCLNHRFRSGFRLAFC--CPWVTPTKEDKLELTPTTSLSTRVNRC 351

Query 376 VRPSDGLPSESGPSSGAPRPGRLPLRNGRVAHHGLPREGPG 417
          + ++ PS +G H P++G G
Sbjct 352 HTKETLFMAGDTAPSEAT-----SGEAGH---PQDGS 381
```

>prf|2118221A cholecystokinin A receptor  
Length=428

Score = 137 bits (346), Expect = 6e-32, Method: Compositional matrix adjust.  
Identities = 107/353 (30%), Positives = 170/353 (48%), Gaps = 61/353 (17%)

```
Query 44 AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD 103
          A+ I+ Y+LIFLL ++GNTLV +++ + M TVTN+F+L+LAVSDL++ +FCMP L+
Sbjct 42 AVQILLYSLIFLLSVLGNTLVITVLINRKRMTVTNIFLLSLAVSDLMCLFCMPFNLI 101

Query 104 NLITGWPFDPNATCKMSGLVQGMVSASVFTLVIAIAVERFRICVHHPFREKL--TLRKALVT 161
          NL+ + F +A CK + G SVS S F LVAI++ER+ I P + ++ T AL
Sbjct 102 NLLKDFIFGSAVCTTTTYFMGTSVSVSTFNLVAISLERYGAICKPLQSRVWQTKSHALKV 161

Query 162 IAVIWAALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKGMRRVYTTVL 221
          IA W L+ IM P + + + +N + C P M++ + T L
Sbjct 162 IAATWCLSFPTIMTPYPI-----YSNLVPFTKNNQNTANMCRFLFPNDVMQSWHTPL 214

Query 222 SHIYLAPLALIVVMYARIARKLCQA-----PGPAPGGE-EAAD----- 258
          ++L P +++V Y I+ +L Q P G+ E+D
Sbjct 215 LILFLIPGIVMMVAYGLISLELYQGIKFEASQKKSAKERKPTSTSSGKYEDSDGCYLQKT 274

Query 259 -----PRASRRRA-----RVVHMLVMVALFFTLISWLPWALL 291
          RA+R R+ RV+ ML+++ + F L W+P+++
Sbjct 275 RPPRKLELRQLSTGSSSRANRIRSNSSAANLMAKKRVIRMLIVIVLFLCWMPIFSANA 334

Query 292 LIDYQLSAPQLHLVTYVYAPFFAHWLAFNNSANPIIYGYNENFRRGFQA 344
          Y SA + ++ F L++ +S PIY + N+ FR GF A F
Sbjct 335 WRAYDTASAER--RLSGTPISFILLLSYISSCMVPIIYCFMNRKFRGLGFMATF 385
```

>gb|AAL26488.1|AF411117\_1 G protein-coupled receptor [Homo sapiens]  
Length=455

Score = 135 bits (340), Expect = 3e-31, Method: Compositional matrix adjust.  
Identities = 85/296 (28%), Positives = 137/296 (46%), Gaps = 45/296 (15%)

```
Query 52 LIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPF 111
          LIF L + GN LV ++V +++ M TVTN+FI +LA+SDLL+ FC+P T++ N+ W
Sbjct 116 LIFALALFGLNALVYVVTTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNISDNWLG 175

Query 112 DNATCKMSGLVQGMVSASVFTLVIAIAVERFRICVHHPFREK--LTLRKALVTIAVIWALA 169
          CKM VQ +V + T+ I AVER + +VHPP+ K T R+A + V+W +A
Sbjct 176 GAFICKMVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMKWQYTNRRFTMLGVVWLVA 235

Query 170 LLIMCP--SAVTLTVTREEHHFMVDARNRSYPLYSWEAWPEKGMRRVYTTVLFSHIYLA 227
          +++ P L + ++ F+ + + C E W +++YTT + S
Sbjct 236 VIVGSPMWHVQQLLEI---KYDFLYEKEH----ICCLEWTSVPVHQKIYTTFILSSSSSC 287

Query 228 PLALIVVMYARIARKLCQAPGAPGGEAADPRASRRRRARVHMLVMVALFFTLISWLPW 287
          L ++ R V M+V V F + W P
Sbjct 288 LLW-----KKKRAVIMMVTVALFAVCWAPPH 314

Query 288 ALLLLIDYQLSAPQLHLVTYVYAPFFAHWLAFNNSANPIIYGYNENFRRGFQA 343
          + ++I+Y + F + F NS NPI+Y + NENE++ +A
Sbjct 315 VVHMIEYSNFEKEYDDVTIKMIFAIVQIIGFSNSICNPIVYAFMNEFKKNVLSA 370
```

>dbj|BAD92474.1| **G** neuropeptide Y receptor Y1 variant [Homo sapiens]  
Length=262

GENE ID: 4886 NPY1R | neuropeptide Y receptor Y1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 127 bits (318), Expect = 9e-29, Method: Compositional matrix adjust.  
Identities = 79/206 (38%), Positives = 116/206 (56%), Gaps = 7/206 (3%)

```
Query 41 PVAAMFIVA--YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMP 98
          P+A +F +A Y + +L + GN + I+LK + M VTN+ I+NL+ SDLLV I C+P
Sbjct 44 PLAMIFTLALAYGAVIILGVSGNLALIIILKQKEMRNVNITLIVNLSFSDLLVAIMCLP 103

Query 99 TTLVDNLITGWPFDPNATCKMSGLVQGMVSASVFTLVIAIAVERFRICVHHPFREKLTLRKA 158
          T V L+ + F A CK++ VQ +S++ S+F+LV I AVER + I++ + R A
Sbjct 104 FTFVYTLMDHWVFGAEMCKLNPFVQCVSITVSIFSLVLI AVERHQLIINPRGWRPNRRHA 163
```

```

Query 159 LVTIAVIWALALLIMCPSAVTLTVTREE-HHFMVDARNRSYPLYSCEWAEWPEKGMRRVYT 217
          V IAVIW LA+ P + +T E + +DA Y C++ +P R YT
Sbjct 164 YVGIAVIWVLAASSLPFLIYQVMTDEPFQNVTLDAYKDK---YVCFDQFPSPDSHRLSYT 220

Query 218 TVLFSHIYLAPLALIVVMYARIARKL 243
          T+L Y PL I + Y ++ RKL
Sbjct 221 TLLLVQLQYFGPLCFIFICYFKV-RKL 245

```

>gb|AAI22552.1| **G** Tachykinin receptor 3 [Homo sapiens]  
Length=465

GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

Score = 125 bits (315), Expect = 2e-28, Method: Compositional matrix adjust.  
Identities = 100/386 (25%), Positives = 172/386 (44%), Gaps = 35/386 (9%)

```

Query 24 ATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFIL 83
          + P NLT + + S A++ +AY ++ + ++GN +V +I+L ++ M TVTN F++
Sbjct 68 SQPWANLT--NQFVQPSWRVALWSLAYGVVAVAVLGNLIVIWII LAHKRMRTVTNYFLV 125

Query 84 NLAVSDDLVLGIFCMPTTLVDNLITGWPFDNATCKMSGLVQGMVSASVFTLVIAIAVERFR 143
          NLA SD + F + L + W F C+ +V AS++++ AIAV+R+
Sbjct 126 NLAFSDASMAAFNTLVNFIYALHSEWYFGANYCRFQNFPPITAVFASIYSMTAIAVDRYM 185

Query 144 CIVHPPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYS- 202
          I+ P ++L+ + I IW LA L+ P + ++ + P +
Sbjct 186 AIIDPLKPRLSATATKIVIGSIWILAFLLAFPQCLY-----SKTKVMPGRTL 232

Query 203 CWEAWPEKGMRR-VYTTVLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRA 261
          C+ WPE + Y ++ +Y PL ++ + Y + L P ++ +
Sbjct 233 CFVQWPEGPKQHFTYHIIIVILVYCFPLIIMGITYTIVGITLWGGEIPGDTCDKYHEQLK 292

Query 262 SRRRARVVMHMLVMVALFFTLWSLPLWALLLLIDYGQLSAPQLHLVTVYAFPAHWAFFN 321
          ++R +VV M+++V + F + WLP +L Q ++ VY F WLA +
Sbjct 293 AKR--KVVKMMIIVVMTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLASF--WLAMSS 348

Query 322 SSANPIIYGYNENFRRGFQAAFRARLCP-----RPSGSHKEAYSERPGGLLH 369
          + NPIIY N+ FR GF+ AF R CP + + H S
Sbjct 349 TMYNPIIYCCLNKRFRAGFKRAF--RWCPIKVVSSYDELELKTTRFHPNRQSSMYTVTRM 406

Query 370 RRVFVVVRPSDGLPSESGPSSGAPR 395
          + VV P+D+ S PR
Sbjct 407 ESMTVVFPDNDADTTRSSRKKRATPR 432

```

>gb|AAB21706.1| **G** neurokinin-3 receptor; NK-3 receptor [Homo sapiens]  
Length=465

GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

Score = 125 bits (314), Expect = 2e-28, Method: Compositional matrix adjust.  
Identities = 100/386 (25%), Positives = 172/386 (44%), Gaps = 35/386 (9%)

```

Query 24 ATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFIL 83
          + P NLT + + S A++ +AY ++ + ++GN +V +I+L ++ M TVTN F++
Sbjct 68 SQPWANLT--NQFVQPSWRVALWSLAYGVVAVAVLGNLIVIWII LAHKRMRTVTNYFLV 125

Query 84 NLAVSDDLVLGIFCMPTTLVDNLITGWPFDNATCKMSGLVQGMVSASVFTLVIAIAVERFR 143
          NLA SD + F + L + W F C+ +V AS++++ AIAV+R+
Sbjct 126 NLAFSDASMAAFNTLVNFIYALHSEWYFGANYCRFQNFPPITAVFASIYSMTAIAVDRYM 185

Query 144 CIVHPPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYS- 202
          I+ P ++L+ + I IW LA L+ P + ++ + P +
Sbjct 186 AIIDPLKPRLSATATKIVIGSIWILAFLLAFPQCLY-----SKTKVMPGRTL 232

Query 203 CWEAWPEKGMRR-VYTTVLFSHIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRA 261
          C+ WPE + Y ++ +Y PL ++ + Y + L P ++ +
Sbjct 233 CFVQWPEGPKQHFTYHIIIVILVYCFPLIIMGITYTIVGITLWGGEIPGDTCDKYHEQLK 292

Query 262 SRRRARVVMHMLVMVALFFTLWSLPLWALLLLIDYGQLSAPQLHLVTVYAFPAHWAFFN 321
          ++R +VV M+++V + F + WLP +L Q ++ VY F WLA +
Sbjct 293 AKR--KVVKMMIIVVMTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLASF--WLAMSS 348

Query 322 SSANPIIYGYNENFRRGFQAAFRARLCP-----RPSGSHKEAYSERPOCLLH 369
          + NPIIY N+ FR GF+ AF R CP + + H S
Sbjct 349 TMYNPIIYCCLNKRFRAGFKRAF--RWCPIKVVSSYDELELKTTRFHPNRQSSMYTVTRM 406

Query 370 RRVFVVVRPSDGLPSESGPSSGAPR 395
          + VV P+D+ S PR
Sbjct 407 ESMTVVFPDNDADTTRSSRKKRATPR 432

```

>emb|CAA46291.1| **G** neuromedin K receptor [Homo sapiens]  
Length=465

GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

Score = 125 bits (314), Expect = 3e-28, Method: Compositional matrix adjust.  
Identities = 95/366 (25%), Positives = 164/366 (44%), Gaps = 33/366 (9%)

```

Query 44 AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDDLVLGIFCMPTTLVD 103
          A++ +AY ++ + ++GN +V +I+L ++ M TVTN F++NLA SD + F +
Sbjct 86 ALWSLAYGVVAVAVLGNLIVIWII LAHKRMRTVTNYFLVNLAFSDASMAAFNTLVNFIY 145

Query 104 NLITGWPFDNATCKMSGLVQGMVSASVFTLVIAIAVERFR CIVHPPFREKLTLRKALVTIA 163
          L + W F C+ +V AS++++ AIAV+R+ I+ P + +L+ + I
Sbjct 146 ALHSEWYFGANYCRFQNFPPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIG 205

Query 164 VIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYS-CWEAWPEKGMRR-VYTTVLF 221
          IW LA L+ P + ++ + P + C+ WPE + Y ++
Sbjct 206 SIWILAFLLAFPQCLY-----SKTKVMPGRTLCFVQWPEGPKQHFTYHIIVI 252

Query 222 SHIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRARVVMHMLVMVALFFTL 281

```

```

      +Y PL ++ + Y + L P ++ + ++R +VV M+++V + F +
Sbjct 253 ILVYCFPLLLIMGITVITVIGITLWGGEIPGDTCDKYHEQLKAKR--KVKMMIIVVMTFAI 310
Query 282 SWLPLWALLLLIDYGQLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQ 341
      WLP +L Q ++ VY F WLA ++ NPIIY N+ FR GF+
Sbjct 311 CWLPYHIYFILTAYIQQQLNRWKYIQQVYLASF--WLAMSSTMYNPIIYCCLNKRFRAGFK 368
Query 342 AAFRRLCP-----RPSGSHKEAYSERPGGLLHRRVVFVVVRPSDGLPSESGP 389
      AF R CP + H S + VV P+D+ S
Sbjct 369 RAF--RWCFFIKVSSYDELELKTTRFHPNRQSSMYTVTRMESMTVVFDPNADTTRSSRK 426
Query 390 SSGAPR 395
      PR
Sbjct 427 KRATPR 432

```

```

>ref|NP_001050.1| [G] tachykinin receptor 3 [Homo sapiens]
sp|P29371.1|NK3R_HUMAN [G] RecName: Full=Neurokinin-3 receptor; Short=NKR; AltName: Full=Neurokinin
B receptor; AltName: Full=NK-3 receptor; Short=NK-3R;
AltName: Full=Tachykinin receptor 3
gb|AAA36366.1| [G] neurokinin-3 receptor
gb|AAR23926.1| [G] tachykinin receptor 3 [Homo sapiens]
gb|AAI21807.1| [G] Tachykinin receptor 3 [Homo sapiens]
gb|EAX06173.1| [G] tachykinin receptor 3 [Homo sapiens]
Length=465

```

```

GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]
(Over 10 PubMed links)
Score = 125 bits (314), Expect = 3e-28, Method: Compositional matrix adjust.
Identities = 95/366 (25%), Positives = 164/366 (44%), Gaps = 33/366 (9%)

```

```

Query 44 AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD 103
      A++ +AY ++ + ++GN +V +I+L ++ M TVTN F++NLA SD + F +
Sbjct 86 ALWSLAYGVVAVAVLGNLIVITLHAKRMRTVTNYFLVNLAFSDASMAAFNTLVNFIY 145
Query 104 NLITGWPFNDATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLTLRKALVTIA 163
      L + W F C+ +V AS+++ AIAV+R+ I+ P + +L+ + I
Sbjct 146 ALHSEWYFGANYCRFQNFPPITAVFASIYSMTAIAVDRYMAIDPLKPRLSATATKIVIG 205
Query 164 VIWALALLIMCPSAVTLTVTREHHFMVDARNRSYPLYS-CWEAWPEKGMRR-VYTTVLF 221
      IW LA L+ P + ++ + P + C+ WPE + Y ++
Sbjct 206 SIWILAFLLAPQCCLY-----SKTKVMPGRTLFCVQWPEGPKQHFTYHIIVI 252
Query 222 SHIYLAPLALIVMYARIARKLCQAPGAPGGEAAADPRASRRRARVHMLVMVALFFTL 281
      +Y PL ++ + Y + L P ++ + ++R +VV M+++V + F +
Sbjct 253 ILVYCFPLLLIMGITVITVIGITLWGGEIPGDTCDKYHEQLKAKR--KVKMMIIVVMTFAI 310
Query 282 SWLPLWALLLLIDYGQLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQ 341
      WLP +L Q ++ VY F WLA ++ NPIIY N+ FR GF+
Sbjct 311 CWLPYHIYFILTAYIQQQLNRWKYIQQVYLASF--WLAMSSTMYNPIIYCCLNKRFRAGFK 368
Query 342 AAFRRLCP-----RPSGSHKEAYSERPGGLLHRRVVFVVVRPSDGLPSESGP 389
      AF R CP + H S + VV P+D+ S
Sbjct 369 RAF--RWCFFIKVSSYDELELKTTRFHPNRQSSMYTVTRMESMTVVFDPNADTTRSSRK 426
Query 390 SSGAPR 395
      PR
Sbjct 427 KRATPR 432

```

```

>gb|AAH95527.1| [G] TACR3 protein [Homo sapiens]
Length=464
GENE ID: 6870 TACR3 | tachykinin receptor 3 [Homo sapiens]
(Over 10 PubMed links)
Score = 124 bits (311), Expect = 7e-28, Method: Compositional matrix adjust.
Identities = 100/386 (25%), Positives = 170/386 (44%), Gaps = 35/386 (9%)

```

```

Query 24 ATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFIL 83
      + P TNLT + + S A + +AY ++ + ++GN +V +I+L ++ M TVTN F++
Sbjct 67 SQPWNLT--NQFVQPSWRIAFWSLAYGVVAVAVLGNLIVITLHAKRMRTVTNYFLV 124
Query 84 NLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMSGLVQGMVSASVFTLVIAIAVERFR 143
      NLA SD + F + L + W F C+ +V AS+++ IAV+R+
Sbjct 125 NLAFSDASMAAFNTLVNFIYALHSEWYFGANYCRFQNFPPITAVFASIYSMTAIAVDRYM 184
Query 144 CIVHPFREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREHHFMVDARNRSYPLYS- 202
      I+ P +L+ + I IW LA L+ P + ++ + P +
Sbjct 185 AIIDPLEPRLSATATKIVIGSIWILAFLLAPQCCLY-----SKTKVMPGRTL 231
Query 203 CWEAWPEKGMRR-VYTTVLFSHIYLAPLALIVMYARIARKLCQAPGAPGGEAAADPRA 261
      C+ WPE + Y ++ +Y PL ++ + Y + L P ++ +
Sbjct 232 CFVQWPEGPKQHFTYHIIVIIILVYCFPLLLIMGITVITVIGITLWGGEIPGDTCDKYHEQLK 291
Query 262 SRRRARVHMLVMVALFFTLWLPLWALLLLIDYGQLSAPQLHLVTVYAFPPFAHWLAFFN 321
      ++R +VV M+++V + F + WLP +L Q ++ VY F WLA +
Sbjct 292 AKR--KVKMMIIVVMTFAICWLPYHIYFILTAYIQQQLNRWKYIQQVYLASF--WLAMS 347
Query 322 SSANPIIYGYNENFRRGFQAARLCP-----RPSGSHKEAYSERPGGLLH 369
      + NPIIY N+ FR GF+ AF R CP + H S
Sbjct 348 TMYNPIIYCCLNKRFRAGFKRAF--RWCFFIKVSSYDELELKTTRFHPNRQSSMYTVTRM 405
Query 370 RRVFVVVRPSDGLPSESGPSSGAPR 395
      + VV P+D+ S PR
Sbjct 406 ESMTVVVFDPNADTTRSSRKKRATPR 431

```

```

>sp|Q13585.1|MTR1L_HUMAN [G] RecName: Full=Melatonin-related receptor; AltName: Full=G protein-coupled
receptor 50; AltName: Full=H9
gb|AAC50614.1| [G] melatonin-related receptor
Length=613

```

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 123 bits (308), Expect = 1e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIFLLC-----MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLV 102
+IF+ C ++GN++V V KN+ + N+F+++L+V+D+LV I+ P L
Sbjct 28 IIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNI FVVSLSVADMLVAIYPYPLMLH 87


Query 103 DNLITGWPFDPNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPPREK--LTLRKALV 160
I GW C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +
Sbjct 88 AMSIGGWDLSQLQCMVGFITGLSVVGSIFNIVAIAINRYCYICHSLQYERIFSVRNTCI 147

Query 161 TIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVL 220
+ + W + +L + P+ T+ D R Y+C + V+T +
Sbjct 148 YLVITWIMTVLAVLPNMYIGTIE-----YDPRT-----YTCIFNYLNNP---VPTVTI 192

Query 221 FSHIYLAPLALIVVMYARIARKLCQAPGAPGEGEAAADPRASRRRARVVHMLVMVALFFT 280
++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHFVLPPLLIVGFCYVRIWTKVLAARDPA-----GQNPDNQLAEVRNFLTMTFVIFLLFA 247

Query 281 LSWLPLWALLLLIDYQGLSAPQLH-LVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRG 339
+ W P+ L +L+ +S ++ + + + A+++A+FNS N +IYG NENFRR
Sbjct 248 VCWCPINVLTVLV---AVSPKEMAGKIPNWLYLAAYFIAYFNSCLNAVIYGLLNENFRRE 304

Query 340 FQAAPRA 346
+ F A
Sbjct 305 YWTIFHA 311
```

>ref|NP\_004215.2|  G protein-coupled receptor 50 [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 123 bits (308), Expect = 1e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIFLLC-----MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLV 102
+IF+ C ++GN++V V KN+ + N+F+++L+V+D+LV I+ P L
Sbjct 28 IIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNI FVVSLSVADMLVAIYPYPLMLH 87



Query 103 DNLITGWPFDPNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPPREK--LTLRKALV 160
I GW C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +
Sbjct 88 AMSIGGWDLSQLQCMVGFITGLSVVGSIFNIVAIAINRYCYICHSLQYERIFSVRNTCI 147

Query 161 TIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVL 220
+ + W + +L + P+ T+ D R Y+C + V+T +
Sbjct 148 YLVITWIMTVLAVLPNMYIGTIE-----YDPRT-----YTCIFNYLNNP---VPTVTI 192

Query 221 FSHIYLAPLALIVVMYARIARKLCQAPGAPGEGEAAADPRASRRRARVVHMLVMVALFFT 280
++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHFVLPPLLIVGFCYVRIWTKVLAARDPA-----GQNPDNQLAEVRNFLTMTFVIFLLFA 247

Query 281 LSWLPLWALLLLIDYQGLSAPQLH-LVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRG 339
+ W P+ L +L+ +S ++ + + + A+++A+FNS N +IYG NENFRR
Sbjct 248 VCWCPINVLTVLV---AVSPKEMAGKIPNWLYLAAYFIAYFNSCLNAVIYGLLNENFRRE 304

Query 340 FQAAPRA 346
+ F A
Sbjct 305 YWTIFHA 311
```

>gb|AAI03697.1|  GPR50 protein [Homo sapiens]  
gb|AAI05684.1|  GPR50 protein [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIFLLC-----MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLV 102
+IF+ C ++GN++V V KN+ + N+F+++L+V+D+LV I+ P L
Sbjct 28 IIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNI FVVSLSVADMLVAIYPYPLMLH 87



Query 103 DNLITGWPFDPNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPPREK--LTLRKALV 160
I GW C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +
Sbjct 88 AMSIGGWDLSQLQCMVGFITGLSVVGSIFNIVAIAINRYCYICHSLQYERIFSVRNTCI 147

Query 161 TIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVL 220
+ + W + +L + P+ T+ D R Y+C + V+T +
Sbjct 148 YLVITWIMTVLAVLPNMYIGTIE-----YDPRT-----YTCIFNYLNNP---VPTVTI 192

Query 221 FSHIYLAPLALIVVMYARIARKLCQAPGAPGEGEAAADPRASRRRARVVHMLVMVALFFT 280
++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHFVLPPLLIVGFCYVRIWTKVLAARDPA-----GQNPDNQLAEVRNFLTMTFVIFLLFA 247

Query 281 LSWLPLWALLLLIDYQGLSAPQLH-LVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRG 339
+ W P+ L +L+ +S ++ + + + A+++A+FNS N +IYG NENFRR
Sbjct 248 VCWCPINVLTVLV---AVSPKEMAGKIPNWLYLAAYFIAYFNSCLNAVIYGLLNENFRRE 304

Query 340 FQAAPRA 346
+ F A
Sbjct 305 YWTIFHA 311
```

>gb|AAI05685.1|  G protein-coupled receptor 50 [Homo sapiens]  
gb|ABY87917.1|  G protein-coupled receptor 50 [Homo sapiens]  
Length=613

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIPLLC-----MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLV 102
      +IF+ C ++GN++V V KN+ + N+F+++L+V+D+LV I+ P L
Sbjct 28 IIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNIFVVSLSVADMLVAIYPYPLMLH 87

Query 103 DNLITGWPFNDATCKMSGVLVQGMVSASVFTLVIAIAVERFCIVHPFREK--LTLRKALV 160
      I GW C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +
Sbjct 88 AMSIGGWDSLQLCQCMVGFIITGLSVVGSIFNIVAIAINRYCYICHSLQYERIFSVRNTCI 147

Query 161 TIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVL 220
      + + W + +L+ P+ T+ D R Y+C + V+T +
Sbjct 148 YLVITWIMTVLAVLPMYIGTIE-----YDPRT-----YTCIFNYLNNP---VFTVTI 192

Query 221 FSHIYLAPLALIVVMYARIARKLCQAPGAPGEGEEAADPRASRRRARVVHMLVMVALFFT 280
      ++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHFVLPPLLIIVGFCYVRIWTKVLAARDPA-----GQNPDNQLAEVRNFLTMTFVIFLLFA 247

Query 281 LSWLPLWALLLLIDYQQLSAPQLH-LVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRG 339
      + W P+ L +L+ +S ++ + + + A+++A+FNS N +IYG NENFR
Sbjct 248 VCWCPINVLTVLV---AVSPKEMAGKIPNWLYLAAYFIAYFNSCLNAVIYGLLENFRRE 304

Query 340 FQAAFRA 346
      + F A
Sbjct 305 YWTIFHA 311
```

>gb|EAW99402.1| **G** G protein-coupled receptor 50 [Homo sapiens]  
Length=617

GENE ID: 9248 GPR50 | G protein-coupled receptor 50 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 83/307 (27%), Positives = 147/307 (47%), Gaps = 35/307 (11%)

```
Query 52 LIPLLC-----MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLV 102
      +IF+ C ++GN++V V KN+ + N+F+++L+V+D+LV I+ P L
Sbjct 28 IIFMFCAMVITIVVDLIGNSMVILAVTKNKKLRNSGNIFVVSLSVADMLVAIYPYPLMLH 87

Query 103 DNLITGWPFNDATCKMSGVLVQGMVSASVFTLVIAIAVERFCIVHPFREK--LTLRKALV 160
      I GW C+M G + G+SV S+F +VAIA+ R+ I H + + ++R +
Sbjct 88 AMSIGGWDSLQLCQCMVGFIITGLSVVGSIFNIVAIAINRYCYICHSLQYERIFSVRNTCI 147

Query 161 TIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVL 220
      + + W + +L+ P+ T+ D R Y+C + V+T +
Sbjct 148 YLVITWIMTVLAVLPMYIGTIE-----YDPRT-----YTCIFNYLNNP---VFTVTI 192

Query 221 FSHIYLAPLALIVVMYARIARKLCQAPGAPGEGEEAADPRASRRRARVVHMLVMVALFFT 280
      ++ PL ++ Y RI K+ A PA +P R + ++ L F
Sbjct 193 VCIHFVLPPLLIIVGFCYVRIWTKVLAARDPA-----GQNPDNQLAEVRNFLTMTFVIFLLFA 247

Query 281 LSWLPLWALLLLIDYQQLSAPQLH-LVTVYAFPPFAHWAFFNSSANPIIYGYNENFRRG 339
      + W P+ L +L+ +S ++ + + + A+++A+FNS N +IYG NENFR
Sbjct 248 VCWCPINVLTVLV---AVSPKEMAGKIPNWLYLAAYFIAYFNSCLNAVIYGLLENFRRE 304

Query 340 FQAAFRA 346
      + F A
Sbjct 305 YWTIFHA 311
```

>ref|NP\_001718.1| **G** bombesin-like receptor 3 [Homo sapiens]

sp|P32247.1|BRS3 HUMAN **G** RecName: Full=Bombesin receptor subtype-3; Short=BRS-3

gb|AAA35604.1| **G** bombesin receptor subtype-3

emb|CAA54031.1| **G** uterine bombesin receptor [Homo sapiens]

emb|CAB10731.1| **G** bombesin-like receptor 3 [Homo sapiens]

gb|AAT79496.1| **G** bombesin-like receptor 3 [Homo sapiens]

gb|EAW88470.1| **G** bombesin-like receptor 3 [Homo sapiens]

Length=399

GENE ID: 680 BRS3 | bombesin-like receptor 3 [Homo sapiens]  
(Over 10 PubMed links)

Score = 122 bits (307), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 83/312 (26%), Positives = 151/312 (48%), Gaps = 17/312 (5%)

```
Query 48 VAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLIT 107
      + YA+I + ++GN ++ + K + M TV N+FI +LA DLL+ + C+P L
Sbjct 52 ITYAVIISVGILGNAILIKVFFKTKSMQTVPNIFITSLAFGDLLELLTLCVPVDATHYLAE 111

Query 108 GWPFNDATCKMSGVLVQGMVSASVFTLVIAIAVERFCIVHPFREKLT--LRKALVTIAVI 165
      GW F CK+ ++ SV SVFTL ++ +R++ +V P + + + K V +
Sbjct 112 GWLFGRIGCKVLSPFIRLTSVGVSVFTLTILSADRYKAVVKPLERQPSNAILKTCVKAGCV 171

Query 166 WALALLIMCPSAVTLTVT--REEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSH 223
      W +++ P A+ V R+ + M SYP+ +K ++ ++ + F
Sbjct 172 WIVSMIFALPEAIFSNVYTFRDPNKNMTFESCTSYPV-----SKLLQEIHSLLCFLV 224

Query 224 IYLAPLALIVVMYARIARKLCQAPGAPGEGEEAADPRASRRRARVVHMLVMVALFFTLSW 283
      Y+ PL++I V Y+ IAR L ++ P E++ + R R+ +++ F L W
Sbjct 225 FYIIPLSIISVYSLIARTLYKSTLNIPTEEQSHARKQIESRKRIARTVLVLVALFALCW 284

Query 284 LPLWALLLLIDYQG---LSAPQLHLTVYAFPPFAHWAFFNSSANPIIYGYNENFRRGF 340
      LP L L + + + H+ + F+ LAF NS NP + +++F++ F
Sbjct 285 LPNHLLYLYHSFTSQTYVDP SAMHFIFTI---FSRVLAFNSNCVNP FALYWLSKSFQKHP 341

Query 341 QAAFRARLCPRP 352
      +A RP
Sbjct 342 KAQLFCCKAERP 353
```

>emb|CAG46720.1| **G** DRD1 [Homo sapiens]



Length=446

GENE ID: 1812 DRD1 | dopamine receptor D1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 146/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCFIVLKNRHMHT-VTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKM 118
          GNTLVC V++ RH+ + VTN F+++LAVSDLLV + MP V + WPF + C +
Sbjct 40 GNTLVCAAVIRFRLRSKVTNFFVISLAVSDLLVAVLVMPWKAVAEIAGWPF-GSFCNI 98


Query 119 SGLVQGMVSASVSFTLVIAIAVERFRFCIVHPFR--EKLTLRKALVTIAIIVALALLI-MCP 175
          M +AS+ L I+V+R+ I PFR K+T + A + I+V W L++LI P
Sbjct 99 WVAFDIMCSTASILNLCVISVDRYWAISSPFYERKMTPKAAPILISVAVTSLVLSIFIP 158

Query 176 SAVTLTVTREEHHFVMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVM 235
          ++ + + +A + + + +C + + R Y + P+A+++V
Sbjct 159 VQLSWHKAKTPSPSDGNATSLAETIDNC----DSSLSRTYAISSSVISFYIPVAIMIVT 213

Query 236 YARIAR-----KLCQAPGPAPGGEEAADPRAS-----RRRARVVHM 271
          Y RI R K CQ E + P +S +R +V+
Sbjct 214 YTRIYRIAQKQIRRIAALERAHAVHAKNCQTTTNGKPVCEQPESSFKMSFKRETKVLKT 273

Query 272 LVMVALFPTLSWLPWALLLLIDYGQLSAPQLHLVTYVYAPFFAHWLAFFNSSANPIIYGY 331
          L ++ F WLP + L ++ + Q + F W + NSS NPIIY
Sbjct 274 LSVIMGVVCWLPFFILNLCILPFCGSGETQPPCIDSNFTDVFVFWGWANSSLNPIIYA- 332

Query 332 FNENFRRGFQAAPRA-RLCP 350
          FN +FR+ F RLCP
Sbjct 333 FNADFRKAFSTLLGCYRLCP 352
```

>ref|NP\_001471.2|  galanin receptor 1 [Homo sapiens]  
Length=349

GENE ID: 2587 GALR1 | galanin receptor 1 [Homo sapiens] (Over 10 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 91/309 (29%), Positives = 154/309 (49%), Gaps = 30/309 (9%)

```
Query 47 IVAYALIFLLCMVGNTLVCFIVLKNR--HMHTVTNMFILNLAVSDLLVGIFCMPTTLVDN 104
          +V + LIF L ++GN+LV ++ +++ + TN+FILNL+++DL +FC+P
Sbjct 37 LVVFLGILFALGVLGNSLVITVLARSKPGKPRSTTNLFILNLSIADLAYLLFCIPFQATVY 96


Query 105 LITGWPFNDATCKMSGLVQGMVSASVSFTLVIAIAVERFRFCIVH--PFREKLTLRKALVTI 162
          + W CK +S+ S+FTL A++V+R+ IVH R AL+ +
Sbjct 97 ALPTWVLGAFICKFIHYFFTVMVLSIFTLAAMSVDYVAIVHSRRSSSLRVSRNALLGV 156

Query 163 AVIWLALALLIMCPSAVTLTVTREEHHFVMDARNRSYPLYSCEAWPEKGMRRVYTTVLFS 222
          IWL++ + P V + F A N+++ CWE WP+ ++ Y F
Sbjct 157 GCIALSLAMASP-----VAYHQGLFHPRASNTQT----CWEQWDPDRHKKAYVVCTFV 206


Query 223 HIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFPTLS 282
          YL PL LI YA++ L + + ++ + + ++V + F +S
Sbjct 207 FGYLPLPLLLICFCYAKVLNHLHKK-----LKNMSKKSEASKKTAQTVLVVVVVFGIS 259

Query 283 WLPLWALLLLIDYGQLSAPQLHLVTYVYAPFF--AHWLAFFNSSANPIIYGYFNENFRRG 339
          WLP + L ++G +T +F F AH LA+ NSS NPIIY + +ENFR+
Sbjct 260 WLPHHIHLWAEFGVFP-----LTPASFLFRITAHCLAYSNSSVNPPIIYAFISENFRKA 313

Query 340 FQAAPFRARL 348
          ++ F+ +
Sbjct 314 YKQVFKCHI 322
```

>sp|P47211.1|GALR1\_HUMAN  RecName: Full=Galanin receptor type 1; AltName: Full=GAL1-R;  
AltName: Full=GALR1

gb|AAA50767.1|  galanin receptor

gb|AAC51936.1|  galanin receptor [Homo sapiens]  
Length=349

GENE ID: 2587 GALR1 | galanin receptor 1 [Homo sapiens] (Over 10 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 91/309 (29%), Positives = 154/309 (49%), Gaps = 30/309 (9%)

```
Query 47 IVAYALIFLLCMVGNTLVCFIVLKNR--HMHTVTNMFILNLAVSDLLVGIFCMPTTLVDN 104
          +V + LIF L ++GN+LV ++ +++ + TN+FILNL+++DL +FC+P
Sbjct 37 LVVFLGILFALGVLGNSLVITVLARSKPGKPRSTTNLFILNLSIADLAYLLFCIPFQATVY 96


Query 105 LITGWPFNDATCKMSGLVQGMVSASVSFTLVIAIAVERFRFCIVH--PFREKLTLRKALVTI 162
          + W CK +S+ S+FTL A++V+R+ IVH R AL+ +
Sbjct 97 ALPTWVLGAFICKFIHYFFTVMVLSIFTLAAMSVDYVAIVHSRRSSSLRVSRNALLGV 156

Query 163 AVIWLALALLIMCPSAVTLTVTREEHHFVMDARNRSYPLYSCEAWPEKGMRRVYTTVLFS 222
          IWL++ + P V + F A N+++ CWE WP+ ++ Y F
Sbjct 157 GCIALSLAMASP-----VAYHQGLFHPRASNTQT----CWEQWDPDRHKKAYVVCTFV 206

Query 223 HIYLAPLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFPTLS 282
          YL PL LI YA++ L + + ++ + + ++V + F +S
Sbjct 207 FGYLPLPLLLICFCYAKVLNHLHKK-----LKNMSKKSEASKKTAQTVLVVVVVFGIS 259

Query 283 WLPLWALLLLIDYGQLSAPQLHLVTYVYAPFF--AHWLAFFNSSANPIIYGYFNENFRRG 339
          WLP + L ++G +T +F F AH LA+ NSS NPIIY + +ENFR+
Sbjct 260 WLPHHIHLWAEFGVFP-----LTPASFLFRITAHCLAYSNSSVNPPIIYAFISENFRKA 313

Query 340 FQAAPFRARL 348
          ++ F+ +
Sbjct 314 YKQVFKCHI 322
```

>emb|CAA41734.1|  D-1 dopamine receptor [Homo sapiens]  
Length=446

GENE ID: 1812 DRD1 | dopamine receptor D1 [Homo sapiens]

(Over 100 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 146/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCFIVLKNRHMHT-VTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKM 118
GNTLVC V++ RH+ + VTN F+++LAVSDLLV + MP V + WPF + C +
Sbjct 40 GNTLVCAAVIRFRLRSKVTNFFVISLAVSDLLVAVLWMPWKAVAEIAGFWPF-GSFCNI 98


Query 119 SGLVQGMVSASVFTLVIAIAVERFRCIVHPFR--EKLTLRKALVTIAVIWALALLI-MCP 175
M +AS+ L I+V+R+ I PFR K+T + A + I+V W L++LI P
Sbjct 99 WVAFDIMCSTASILNLCVISVDRYWAISSPFRYERKMTPKAAFILISVAVTSLVLSIFIP 158


Query 176 SAVTLTVTREEHHFVMDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVM 235
++ + +A + + + +C + + R Y + P+A+++V
Sbjct 159 VQLSWHKAKPTSPSDGNATSLAETIDNC-----DSSLRTYAISSSVISFYIPVAIMIVT 213


Query 236 YARIAR-----KLCQAPGPAPGGEAAADPRAS-----RRRARVVHM 271
Y RI R K CQ E + P +S +R +V+
Sbjct 214 YTRIYRIAQKQIRRIALERAHAVHAKNCQTTTGNKGKPEVCSQPESSEFKMSFKRETKVLKT 273


Query 272 LVMVALFFTLWSLWALLLLIDYQQLSAPQLHLVTYVYAPFFAHWLAFNSSANPIIYGY 331
L ++ F WLP + L ++ + Q + F W + NSS NPIIY
Sbjct 274 LSVIMGVFVCCWLPFFILNLCILPFCGSGETQPFCDISNTFDVFWFVGWANSNLNPIIYA- 332


Query 332 FNENFRRGFQAAPRA-RLCP 350
FN +FR+ F RLCP
Sbjct 333 FNADFRKAFSTLLGCYRLCP 352
```


>gb|AAK83235.1|AF343725.1  G-protein-coupled receptor GPR54 [Homo sapiens]

dbj|BAB55446.1|  G protein-coupled receptor [Homo sapiens]

gb|AAK33126.1|  putative G protein-coupled receptor [Homo sapiens]

gb|AAP82929.1|  hypogonadotropin-1 [Homo sapiens]

gb|EAW69583.1|  KISS1 receptor [Homo sapiens]

gb|AAI40826.1|  KISS1 receptor [Homo sapiens]  
Length=398

GENE ID: 84634 KISS1R | KISS1 receptor [Homo sapiens] (Over 10 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 104/351 (29%), Positives = 168/351 (47%), Gaps = 29/351 (8%)

```
Query 9 PNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCMVGNLTVCFIV 68
PN+SW N + A N + + A + + +A + LL +VGN+LV +++
Sbjct 9 PNASWGA PANASGCGPGCA-NASDGPVPSRAVDWLVLFFAALMLLGLVGNLSLVIYVI 67


Query 69 LKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMSGLVQGMVS 128
+++ M TVTN +I NLA +D+ + C+P T + + GW + CK +Q +SV
Sbjct 68 CRHKPMRTVTNFIYANLAATDVTFLLCCVPFTALLYPLPGWVLGDFMCKFVNYIQVSVQ 127

Query 129 ASVFTLVIAIAVERFRCIVHPFR--EKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREE 186
A+ TL A++V+R+ V P R + T R AL IW + + SA L + R
Sbjct 128 ATCATLTAMSDVRWYVTFPLRALHRRTPRLALAVSLSIWVGSAAV---SAPVLALHR-- 182

Query 187 HHFVMDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARKLCQ- 245
+ R+Y C EA+P + + R + +YL PL YA + R L +
Sbjct 183 ----LSPGPRAY---CSEAFPSRALERAFALYNLLALYLLPLLATCACYAAMLRHLGRV 234

Query 246 APGPAPG-----GEEAADPRASRRRARVVHMLVMVALFFTLWSLWALLLLIDYQQLSA 300
A PAP G+ A+ RA RA+V ++ V L F W P + L+L G +
Sbjct 235 AVRPAADSAIQQLAE-RAGAVRAKVSRLVAAVVLFFAACWGPIQLFLVLQALGPAGS 293

Query 301 PQLHLVTYVYAPF-FAHWLAFNSSANPIIYGYFNENFRRGFQAAPRARLCP 350
YA +AH +++ NS+ NP++Y + +FR+ F+ R+CP
Sbjct 294 WHPRSYAAYALKTWAHMSYSNSALNPLLYAFLGSHFRQAFR-----RVCP 339
```

>gb|EAW61376.1|  dopamine receptor D1, isoform CRA\_a [Homo sapiens]  
Length=469

GENE ID: 1812 DRD1 | dopamine receptor D1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 146/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCFIVLKNRHMHT-VTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKM 118
GNTLVC V++ RH+ + VTN F+++LAVSDLLV + MP V + WPF + C +
Sbjct 63 GNTLVCAAVIRFRLRSKVTNFFVISLAVSDLLVAVLWMPWKAVAEIAGFWPF-GSFCNI 121


Query 119 SGLVQGMVSASVFTLVIAIAVERFRCIVHPFR--EKLTLRKALVTIAVIWALALLI-MCP 175
M +AS+ L I+V+R+ I PFR K+T + A + I+V W L++LI P
Sbjct 122 WVAFDIMCSTASILNLCVISVDRYWAISSPFRYERKMTPKAAFILISVAVTSLVLSIFIP 181


Query 176 SAVTLTVTREEHHFVMDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVM 235
++ + +A + + + +C + + R Y + P+A+++V
Sbjct 182 VQLSWHKAKPTSPSDGNATSLAETIDNC-----DSSLRTYAISSSVISFYIPVAIMIVT 236


Query 236 YARIAR-----KLCQAPGPAPGGEAAADPRAS-----RRRARVVHM 271
Y RI R K CQ E + P +S +R +V+
Sbjct 237 YTRIYRIAQKQIRRIALERAHAVHAKNCQTTTGNKGKPEVCSQPESSEFKMSFKRETKVLKT 296












Query 272 LVMVALFFTLWSLWALLLLIDYQQLSAPQLHLVTYVYAPFFAHWLAFNSSANPIIYGY 331
L ++ F WLP + L ++ + Q + F W + NSS NPIIY
Sbjct 297 LSVIMGVFVCCWLPFFILNLCILPFCGSGETQPFCDISNTFDVFWFVGWANSNLNPIIYA- 355

Query 332 FNENFRRGFQAAPRA-RLCP 350
FN +FR+ F RLCP
Sbjct 356 FNADFRKAFSTLLGCYRLCP 375
```

>ref|NP\_000785.1|  dopamine receptor D1 [Homo sapiens]

sp|P21728.1|DRD1\_HUMAN  RecName: Full=D(1A) dopamine receptor






gb|AAM18131.1|AF498961.1  dopamine receptor D1 [Homo sapiens]  
11 more sequence titles

emb|CAA39286.1|  dopamine receptor D1 [Homo sapiens]  
emb|CAA39284.1|  dopamine D1 receptor [Homo sapiens]  
gb|AAB26273.1|  dopamine D1 receptor; DA D1 receptor [Homo sapiens]  
dbj|BAC05902.1|  seven transmembrane helix receptor [Homo sapiens]  
gb|AAH74979.1|  Dopamine receptor D1 [Homo sapiens]  
gb|AAH74978.1|  Dopamine receptor D1 [Homo sapiens]  
gb|AAH96837.1|  Dopamine receptor D1 [Homo sapiens]  
gb|EAW61377.1|  dopamine receptor D1, isoform CRA\_b [Homo sapiens]  
dbj|BAG36741.1|  unnamed protein product [Homo sapiens]  
prf||1614341A  dopamine receptor D1  
prf||1614342A  dopamine D1 receptor  
Length=446

GENE ID: 1812 DRD1 | dopamine receptor D1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 122 bits (306), Expect = 2e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 146/320 (45%), Gaps = 36/320 (11%)


Query	60	GNTLVCFIVLKNRRMHT-VTNMFILNLAVSDLLVGIFCMTTLVDNLITGWPF DNATCKM	118
		GNTLVC V++ RH+ + VTN F+++LAVSDLLV + MP V + WPF + C +	
Sbjct	40	GNTLVCAAVIRFRLRSKVTNFFVISLAVSDLLVAVLVMPWKAVAEIAGFWPF-GSFCNI	98
Query	119	SGLVQGMVSASVFTLVIAVERFRICIVHPER--EKLTLRKALVTIAVIWALALLI-MCP	175
		M +AS+ L I+V+R+ I PFR K+T + A + I+V W L++LI P	
Sbjct	99	WVAFDIMCSTASILNLCVISVDRYWAISSPFYERKMTPKAAFILISVAWTLISLVISFIP	158
Query	176	SAVTLTVTREHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVM	235
		++ + + +A + + + +C + + R Y + P+A+++V	
Sbjct	159	VQLSWHKAKTPSPDGNATSLAETIDNC-----DSSLRTYAISSSVISFYIPVAIMIVT	213
Query	236	YARIAR-----KLCQAPGPAPGEEAADPRAS-----RRRARVVHM	271
		Y RI R K CQ E + P +S +R +V+	
Sbjct	214	YTRIYRIAQKQIRRIAALERAHAVHAKNCQTTGNGKPVCECSQPESSEFKMSFKRETKVLKT	273
Query	272	LVMVALFFTLWSLPLWALLLLIDYQLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGY	331
		L ++ F WLP + L ++ + Q + F W + NSS NPIIY	
Sbjct	274	LSVMGMVFVCCWLPFFLILNLCILPFCGSGETQPPCIDSNTFDVFWFVGWANSNLPPIIYA-	332
Query	332	FNENFRRGFQAFAFR-RLCP 350	
		FN +FR+ F RLCP	
Sbjct	333	FNADFRKAFSTLLGCYRLCP 352	


>gb|AAB60356.1|  galanin receptor  
gb|AAC95397.1|  galanin receptor [Homo sapiens]  
gb|AAS47032.1|  galanin receptor 1 [Homo sapiens]  
gb|AAH95530.1|  Galanin receptor 1 [Homo sapiens]  
gb|EAW66603.1|  galanin receptor 1 [Homo sapiens]  
Length=349





GENE ID: 2587 GALR1 | galanin receptor 1 [Homo sapiens] (Over 10 PubMed links)

Score = 122 bits (306), Expect = 3e-27, Method: Compositional matrix adjust.  
Identities = 91/309 (29%), Positives = 154/309 (49%), Gaps = 30/309 (9%)

Query	47	IVAYALIFLLCMVGNTLVCFIVLKNR--HMHTVTNMFILNLAVSDLLVGIFCMTTLVDN	104
		+V + LIF L ++GN+LV ++ ++ + TN+FILNL+++DL +FC+P	
Sbjct	37	LVVVGLIFALGVLGNSLVITVLARSKPGKPRSTNLFILNLSIADLAYLLFCIPFQATVY	96
Query	105	LITGWPF DNATCKMSSGLVQGMVSASVFTLVIAVERFRICIVH--PFREKLTLRKALVTI	162
		+ W CK +S+ S+FTL A++V+R+ IVH R AL+ +	
Sbjct	97	ALPTWVLGAFICKFIHYFFTVMVLSIPTLAAMSVDYVAIVHSRRSSSLRVSRNALLGV	156
Query	163	AVIWAALLIMCPSAVTLTVTREHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLF	222
		IWAL++ + P V + F A N+++ CWE WP+ ++ Y F	
Sbjct	157	GCIWALSIAMASP-----VAYHQGLFHPRASNQTF----CWEQWDPDRHKKAYVVCTFV	206
Query	223	HIYLAPLALIVVMYARIARKLCQAPGPAPGEEAADPRASRRRARVVHMLVMVALFFTL	282
		YL PL LI YA++ L + + + + + ++V + F +S	
Sbjct	207	FGYLLPLLLICFCYAKVLNHLHKK-----LKNMSKKSEASKKTAQTVLVVVVVGIS	259
Query	283	WLPWALLLLIDYQLSAPQLHLVTVYAFPP---AHWLAFFNSSANPIIYGYFNENFRRG	339
		WLP + L ++G +T +F F AH LA+ NSS NPIIY + +ENFR+	
Sbjct	260	WLPHHIHLWAEFGVFP-----LTPASFLFRITACHLAYSNSSVNPIIYAFLENFRKA	313
Query	340	FQAAPFRARL 348	
		++ F+ +	
Sbjct	314	YKQVFKCHI 322	

>ref|NP\_115940.2|  G protein-coupled receptor 54 [Homo sapiens]

sp|Q969F8.2|KISSR HUMAN  RecName: Full=KiSS-1 receptor; Short=KiSS-1R; AltName: Full=Kisspeptins receptor; AltName: Full=Metastin receptor; AltName: Full=G-protein coupled receptor 54; AltName: Full=Hypogonadotropin-1; Short=hOT7T175

emb|CAC40817.1|  G protein-coupled receptor [Homo sapiens]  
gb|AAP82930.1|  hypogonadotropin-1 [Homo sapiens]  
gb|AAI41813.1|  KISS1 receptor [Homo sapiens]  
gb|ACG60651.1|  KISS1 receptor [Homo sapiens]  
Length=398

GENE ID: 84634 KISS1R | KISS1 receptor [Homo sapiens] (Over 10 PubMed links)

Score = 122 bits (305), Expect = 3e-27, Method: Compositional matrix adjust.  
Identities = 104/351 (29%), Positives = 168/351 (47%), Gaps = 29/351 (8%)

```
Query 9 PNSSWPLSQNGTNTATPATNLTFSYYQHTSPVAAMFIVAYALIFLLCMVGNLTVCFIV 68
PN+SW N + A N + A + + +A + LL +VGN+LV +++
Sbjct 9 PNASWGAPANASGCGPCGA-NASDGPVPSRAVDWLVLFFAALMLLGLVGNLSLVIYVI 67

Query 69 LKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKMSGLVQGMVS 128
+++ M TVTN +I NLA +D+ + C+P T + + GW + CK +Q +SV
Sbjct 68 CRHKPMRTVTNFIYANLAATDVTFLLCCVPFTALLYPLPGWVLGDFMCKFVNYIQVSVQ 127

Query 129 ASVFTLVIAIAVERFCIVHPFR--EKLTLRKALVTIAVIWALALLIMCPSAVTLTVTREE 186
A+ TL A++V+R+ V P R + T R AL IW + + SA L + R
Sbjct 128 ATCATLTAMSVDRIYVTFPLRALHRRTPRLALAVSLSIWVGSAAV---SAPVLALHR-- 182

Query 187 HHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIARKLCQ- 245
+ R+Y C EA+P + + R + +YL PL YA + R L +
Sbjct 183 ---LSPGPRAY---CSEAPPSRALERAFALYNLLALYLPLLATCACYAAMLRHLGRV 234

Query 246 APGPAPG-----GEEAADPRASRRRVRVHMLVMVALFFTLWSLPLWALLLLIDYQQLSA 300
A PAP G+ A+ RA RA+V ++ V L F W P+ +L+L G +
Sbjct 235 AVRPAPADSAQQGVLAERAGAVRAKVSRLVAAVVLPAACWGPQLFLVLQALGPAGS 293

Query 301 PQLHLVTVYAFPF-FAHWLAFFNSSANPIIYGYPFNENFRRGFQAARLCP 350
YA +AH +++ NS+ NP++Y + +FR+ F+ R+CP
Sbjct 294 WHPRSYAAYALKTWAHCHMSYSNSALNPLLYAFLGSHFRQAFR----RVCP 339
```

>prf|1614340A dopamine receptor D1  
Length=446

Score = 120 bits (302), Expect = 6e-27, Method: Compositional matrix adjust.  
Identities = 94/320 (29%), Positives = 145/320 (45%), Gaps = 36/320 (11%)

```
Query 60 GNTLVCFIVLKNRHMHT-VTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCKM 118
GNTLVC V++ RH+ VTN F+++LAVSDLLV + MP V + WPF + C +
Sbjct 40 GNTLVCAAVIRFRHLRSKVTNFFVISLAVSDLLVAVLVMWPWKAIEIAGWPF-GSFCNI 98


Query 119 SGLVQGMVSASVFTLVIAIAVERFCIVHPFR--EKLTLRKALVTIAVIWALALLI-MCP 175
M +AS+ L I+V R+ I PFR K+T + A + I+V W L++LI P
Sbjct 99 WVAFDIMCSTASILNLCVISVNRWATSSPFYERKMTPKAAFILISVAVTSLVLSIFIP 158

Query 176 SAVTLTVTREEHHFMVDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAPLALIVVM 235
++ +A + + + +C + + R Y + P+A+++V
Sbjct 159 VQLSWHKAKPTSPSDGNATSLAETIDNC-----DSSLRTYAISSSVISFYIPVAIMIVT 213

Query 236 YARIAR-----KLCQAPGPAPGEEAADPRAS-----RRRARVVMH 271
Y RI R K CQ E + P +S +R +V+
Sbjct 214 YTRIYRIAQKQIRRIALERAHAVHAKNCQTTTNGKPVCECSQPESSEFKMSFKRETKVLKT 273

Query 272 LVMVALFFTLWSLPLWALLLLIDYQQLSAPQLHLVTVYAFPF-FAHWLAFFNSSANPIIYG 331
L ++ F WLP + L ++ + Q + F W + NSS NPIIY
Sbjct 274 LSVIMGVFVCCWLPFFILNLCILPFCGSGETQPPCIDSNTFNVFVWFGWANSSLNPIIYA- 332

Query 332 FNENFRRGFQAARFRA-RLCP 350
FN +FR+ F RLCP
Sbjct 333 FNADFRKAFSTLLGCYRLCP 352
```

>dbj|BAG36078.1|  unnamed protein product [Homo sapiens]  
Length=370

GENE ID: 2834 PRLHR | prolactin releasing hormone receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 117 bits (294), Expect = 5e-26, Method: Compositional matrix adjust.  
Identities = 100/305 (32%), Positives = 153/305 (50%), Gaps = 25/305 (8%)

```
Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI-TGWPFNDATCKM 118
GN L+ ++ + R +H VTN+ I NLA+SD+L+ C+P TL GW F C +
Sbjct 77 GNCLLVLVIAVRRLHNVTNLLIGNLALSDVLMCTACVPLTLAYAFEPRGWVFGGLCHL 136


Query 119 SGLVQGMVSASVFTLVIAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAV 178
+Q ++V SVFTL IAV+R+ +VHP R +++LR + + IWAL+ ++ P+AV
Sbjct 137 VFFLPQPTVTVSVFTLTITIAVDRIYVVLVHPLRRRISRLRSAYAVLAIWALSAVLALPAV 196


Query 179 TLTVTREEHHFMVDARNRSYPLYSCEAW-PEKGMRRVYTTVLFSHIYLAPLALIVMYA 237
H + V+ + L C E W ++ R++Y L YL PL +I++ Y
Sbjct 197 -----HTYHVELKPHDVRL--CEEFWGSQERQQLYAWGLLLVTVLLPLLVILLVSYV 246

Query 238 RIARKLCQAPGPAPGEEAADPRASRRRVRVHMLVMVALFFTLWSLPLWALLLLIDYQG 297
R++ KL P + AD +RRR +LV+V + F + WLPL LL D
Sbjct 247 RVSVKLRNRVPGCVTQSQADWDRAARRRRTFC-LLVVVVVFAVCWLPVHVFNLLRDLD 305


Query 298 LSAPQLHLVTVYAFPF---FAHWLAFFNSSANPIIYGYPFNENFRRGFQAARLCP 353
H + YAF HWA ++ NP IY + +++PR + A PR
Sbjct 306 -----HAIDPYAFGLVQLLCHWLMSSACYNPFIYAWLHDSFREELRKLVAW--PRKI 357


Query 354 GSHKE 358
H +
Sbjct 358 APHGQ 362
```


>ref|NP\_001041.1|  somatostatin receptor 2 [Homo sapiens]  
13 more sequence titles

sp|P30874.1|SSR2 HUMAN  RecName: Full=Somatostatin receptor type 2; AltName: Full=SS2R;  
AltName: Full=SRIF-1

gb|AAF42809.1|AF184174\_1  somatostatin receptor 2A [Homo sapiens]

gb|AAA58248.1|  somatostatin receptor isoform 2

gb|AAH19610.1|  Somatostatin receptor 2 [Homo sapiens]

dbj|BAC06126.1|  seven transmembrane helix receptor [Homo sapiens]

gb|AAO92064.1| **G** somatostatin receptor 2 [Homo sapiens]  
 gb|AAV38729.1| **G** somatostatin receptor 2 [Homo sapiens]  
 gb|AAH95495.1| **G** Somatostatin receptor 2 [Homo sapiens]  
 gb|EAW89112.1| **G** somatostatin receptor 2, isoform CRA\_b [Homo sapiens]  
 dbj|BAF83434.1| **G** unnamed protein product [Homo sapiens]  
 Length=369

GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 117 bits (293), Expect = 8e-26, Method: Compositional matrix adjust.  
 Identities = 98/376 (26%), Positives = 170/376 (45%), Gaps = 44/376 (11%)

Query 1 MEGEPSQPPNS--SWPLSQNGTNTTEATPATNLTFSYYQHTSPVAAMFIVAYALIFLLCM 58  
 M EP ++ S P NG+ +T +N T YY TS FI +L LC  
 Sbjct 3 MADEPLNGSHTWLSIPFDLNGS-VVSTNTSNQT-EPYDLTSTNAVLTFIYFVVCIIIGLC- 59

Query 59 VGNTLVCFIVLKNRHHMTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKM 118  
 GNTLV ++L+ M T+TN++ILNLAV+D L + +P + + WPF A C++  
 Sbjct 60 -GNTLVIYVILRYAKMKTITNIYILNLAIADLFL-MLGLPFLAMQVALVHWPFGKAICRV 117

Query 119 SGLVQGMVSASVFTLVIAIAVERFRFCIVHPPREKLTLR---KALVTIAVIWALALLIMCP 175  
 V G++ S+F L +++R+ +VHP + R + +T+AV W ++LL++ P  
 Sbjct 118 VMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRPTAKMITMAV-WGVSLLVILP 176

Query 176 SAVTLTVTREEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHI--YLAPLALIV 233  
 + R+ + SC WP + + +++ I +L PL +I  
 Sbjct 177 IMI-----YAGLRSNQWGRSSCTINWPGESGAWYTGFIYTFILGFLVPLTIIC 225

Query 234 VMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALFPTLSWLPWALLLLI 293  
 + Y I K+ G + + +V M+ +V F WLP + +  
 Sbjct 226 LCYLLFIITKV-----KSSGIRVSGSKRKKSEKVTMRVSIIVAVFIFCWLFPY----IF 275

Query 294 DYGQLS-----APQLHLVTVYAFPPAHWLAFFNSSANPIIYGYNENFRRGFQAAF-RAR 347  
 + +S P L + F F L + NS ANPI+Y + +NF++ FQ +  
 Sbjct 276 NVSSVSMAISPTPALKGM---FDFVVVLTYANSCANPILYAFLSDNFKSFQNVLCCLVK 331

Query 348 LCPRPSGSHKEAYSER 363  
 + G ++ ++  
 Sbjct 332 VSGTDDGERSDSKQDK 347

>gb|AAA20828.1| **G** somatostatin receptor  
 Length=363

GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 117 bits (293), Expect = 8e-26, Method: Compositional matrix adjust.  
 Identities = 94/312 (30%), Positives = 148/312 (47%), Gaps = 40/312 (12%)

Query 60 GNTLVCFIVLKNRHHMTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMS 119  
 GNTLV ++VL+ M TVTN++ILNLAV+D+L + +P N + WPF C++  
 Sbjct 57 GNTLVIYVVLRFAMKMTVTNIYILNLAVADVLY-MLGLPFLATQNAASFVPGPVLCLRV 115

Query 120 GLVQGMVSASVFTLVIAIAVERFRFCIVHPPREKLTLRKALVTI--AVIWAALLIMCPSA 177  
 + G++ SVF L ++V+R+ +VHP R + + A W L+L + P  
 Sbjct 116 MTLDGVNQFTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLASAAWVLSLCLMSLPLL 175

Query 178 VTLTVTREEHHFMDARNRSYPLYSCEAWPE-----KGMRRVYTTVLFSHIYLAFLALI 232  
 V V +C +WPE + +YT VL + APL +I  
 Sbjct 176 VFADVQEGG-----TCNASWPEPVGLWGAVFIITYTAVLG--FFAPLLVI 217

Query 233 VMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALFPTLSWLPWALLLLI 292  
 + Y I K+ A G R S R +V M++V L F WLP + + ++  
 Sbjct 218 CLCYLLIIVVKV---RAAGVRVGCVRRRSER--KVTRMVLVVLVLFAGCWLPFFVTNIV 270

Query 293 IDYQQLSAPQLHLVTVYAFPPAHWLAFFNSSANPIIYGYNENFRRGFQAAFRLCPRP 352  
 ++ PQ + + F L++ NS ANP++YG+ ++NFR+ FQ LC R  
 Sbjct 271 --NLAVALPQ-EPASAGLYFFVILSYANSCANPVLYGFLSDNFRQSFQKV---LCLRK 323

Query 353 GSGHKEAYSERP 364  
 K+A + P  
 Sbjct 324 GSGAKDADATEP 335

>ref|NP\_001044.1| **UG** somatostatin receptor 5 [Homo sapiens]  
 sp|P35346.3|SSR5 HUMAN **G** RecName: Full=Somatostatin receptor type 5; AltName: Full=SS5R  
 dbj|BAA04107.1| **G** fifth somatostatin receptor subtype [Homo sapiens]  
 gb|AAB31829.1| **G** somatostatin receptor subtype SSTR5, SRIF receptor subtype SSTR5  
 [human, Peptide, 364 aa]  
 gb|AAL88744.1| **G** somatostatin receptor subtype 5 [Homo sapiens]  
 gb|EAW85687.1| **G** somatostatin receptor 5 [Homo sapiens]  
 Length=364

GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 117 bits (293), Expect = 9e-26, Method: Compositional matrix adjust.  
 Identities = 94/312 (30%), Positives = 148/312 (47%), Gaps = 40/312 (12%)

Query 60 GNTLVCFIVLKNRHHMTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDPNATCKMS 119  
 GNTLV ++VL+ M TVTN++ILNLAV+D+L + +P N + WPF C++  
 Sbjct 57 GNTLVIYVVLRFAMKMTVTNIYILNLAVADVLY-MLGLPFLATQNAASFVPGPVLCLRV 115

Query 120 GLVQGMVSASVFTLVIAIAVERFRFCIVHPPREKLTLRKALVTI--AVIWAALLIMCPSA 177  
 + G++ SVF L ++V+R+ +VHP R + + A W L+L + P  
 Sbjct 116 MTLDGVNQFTSVFCLTVMSVDRYLAVVHPLSSARWRRPRVAKLASAAWVLSLCLMSLPLL 175

Query 178 VTLTVTREEHHFMDARNRSYPLYSCEAWPE-----KGMRRVYTTVLFSHIYLAFLALI 232  
 V V +C +WPE + +YT VL + APL +I  
 Sbjct 176 VFADVQEGG-----TCNASWPEPVGLWGAVFIITYTAVLG--FFAPLLVI 217

```

Query 233 VVMYARIARKLCQAPGPAGGEEAADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLL 292
          + Y I K+ A G R S R +V M+++V L F WLP + + ++
Sbjct 218 CLCYLLIVVKV-----RAAGVRVGCVRRRSER--KVTRMVLVVVLVFGCWLFPFTVNIV 270

Query 293 IDYGQLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRP 352
          ++ PQ + + F L++ NS ANP++YG+ ++NFR+ FQ LC R
Sbjct 271 --NLAVALPQ-EPASAGLYFFVVILSYANSCANPVLYGFLSDNFRQSPQKV---LCLRK 323

Query 353 GSGHKEAYSERP 364
          K+A + - P
Sbjct 324 GSGAKDADATEP 335

```

```

>ref|NP_004239.1| UG G protein-coupled receptor 10 [Homo sapiens]
sp|P49683.2|PRLHR HUMAN G RecName: Full=Prolactin-releasing peptide receptor; Short=PrRP
receptor; Short=PrRPR; AltName: Full=G-protein coupled receptor
10; Short=hGR3
dbj|BAA31159.1| G human prolactin-releasing peptide receptor [Homo sapiens]
8 more sequence titles

```

```

dbj|BAB83030.1| G prolactin releasing peptide receptor [Homo sapiens]
gb|AAH95539.1| G PRLHR protein [Homo sapiens]
gb|AAI01491.1| G PRLHR protein [Homo sapiens]
gb|AAI01493.1| G PRLHR protein [Homo sapiens]
gb|EAW49413.1| G prolactin releasing hormone receptor, isoform CRA_a [Homo sapiens]
gb|EAW49414.1| G prolactin releasing hormone receptor, isoform CRA_a [Homo sapiens]
gb|ABQ52422.1| G prolactin releasing hormone receptor [Homo sapiens]
dbj|BAF83150.1| G unnamed protein product [Homo sapiens]
Length=370

```

```

GENE ID: 2834 PRLHR | prolactin releasing hormone receptor [Homo sapiens]
(Over 10 PubMed links)

Score = 117 bits (292), Expect = 9e-26, Method: Compositional matrix adjust.
Identities = 100/305 (32%), Positives = 152/305 (49%), Gaps = 25/305 (8%)

```

```

Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI-TGWPFDNATCKM 118
          GN L+ ++ + R +H VTN I NLA+SD+L+ C+P TL GW F C +
Sbjct 77 GNCLLVLVIAVRRLHNVNTNFIIGNLALSDVLMCTACVPLTLAYAFEPGRGWVFGGLCHL 136

Query 119 SGLVQGMVSASVFTLVAIAVERFCIVHPFREKLTLRKALVTIAVIWALALLIMCPSAV 178
          +Q ++V SVFTL IAV+R+ +VHP R +++LR + + IWAL+ ++ P+AV
Sbjct 137 VFFLQPVTVYVSVFTLTITIAVDYVVLVHPLRRRISRLSAYAVLAIWALSAVLALPAAV 196

Query 179 TLTVTREEHHFMDARNRSYPLYSCEAW-PEKGMRRVYTTVLFSHIYLAFLALIVMYA 237
          H + V+ + + L C E W + + R++Y L YL PL +I++ Y
Sbjct 197 -----HTHVELKPHDVRLL--CEEPWGSQERQRLYAWGLLLVTVLLPLLVILLSYV 246

Query 238 RIARKLCQAPGPAGGEEAADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLIDYQG 297
          R++ KL P + AD +RRR +LV+V + F + WLPL LL D
Sbjct 247 RVSVKLNRNVVPGCVTQSQADWDARRRRRTFC-LLVVVVVFAVCWLPFHVFNLLRDLDLP 305

Query 298 LSAPQLHLVTVYAFP----FAHWLAFFNSSANPIIYGYNENFRRGFQAAFRARLCPRPS 353
          H + YAF HwLA ++ NP IY + +++PR + A PR
Sbjct 306 -----HAIDPYAFGLVQLLCHWLAMSSACYNPFYIYAWLHDSFREELRKLLVAW--PRKI 357

Query 354 GSHKE 358
          H +
Sbjct 358 APHGQ 362

```

```

>gb|AAF42810.1|AF184174.2 G somatostatin receptor 2B [Homo sapiens]
gb|EAW89111.1| G somatostatin receptor 2, isoform CRA_a [Homo sapiens]
Length=356

GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]
(Over 10 PubMed links)

Score = 116 bits (291), Expect = 1e-25, Method: Compositional matrix adjust.
Identities = 97/353 (27%), Positives = 163/353 (46%), Gaps = 43/353 (12%)

```

```

Query 1 MEGEPSQPPNS--SWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVAYALIFLLCM 58
          M EP ++ S P NG+ +T +N T YY TS FI I LC
Sbjct 3 MADEPLNGSHTWLSIPDLNGS-VVSTNTSNQT-EPYDYLTSNAVLTFIYFVVCIIIGLC- 59

Query 59 VGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLIITGWPFDNATCKM 118
          GNTLV +++L+ M T+TN++ILNLA++D L + +P + + WPF A C++
Sbjct 60 -GNTLVIVILRYAKMKTITINIIYILNLAIADELFLMLGLPFLAMQVALVHWPFKAICRV 117

Query 119 SGLVQGMVSASVFTLVAIAVERFCIVHPFREKLTLR---KALVTIAVIWALALLIMCP 175
          V G++ S+F L +++R+ +VHP + R ++T+AV W ++LL++ P
Sbjct 118 VMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKWRPRPTAKMITMAV-WGVSLVLVILP 176

Query 176 SAVTLTVTREEHHFMDARNRSYPLYSCEAWPEKGMRRVYTTVLFSHI--YLAPLALIV 233
          + R+ + SC WP + ++++ I +L PL +I
Sbjct 177 IMI-----YAGLRSNQWGRSSCTINWPGESGAWYTGFIYTFILGFLVPLTIIC 225

Query 234 VMYARIARKLCQAPGPAGGEEAADPRASRRRARVVHMLVMVALFFTLISWLPWALLLLL 293
          + Y I K+ G + + +V M+ +V F WLP + + +
Sbjct 226 LCYLFIIIKV-----KSSGIRVGSSKKRKKSEKVVTRMVSIVVAVFIFCWLPPY---IF 275

Query 294 DYQGLS----APQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQ 341
          + +S P L + F F L + NS ANPI+Y + ++NF++ FQ
Sbjct 276 NVSSVSMASPTPALKGM---FDFVVVLTANSANPILYAFSLDNFKKSFQ 324

```

```

>ref|NP_658986.1| UG prokineticin receptor 2 [Homo sapiens]
sp|Q8NFJ6.1|PKR2 HUMAN G RecName: Full=Prokineticin receptor 2; Short=PK-R2; AltName:
Full=G-protein coupled receptor 73-like 1; AltName: Full=GPR73b;

```

AltName: Full=GPRg2

gb|AAM48128.1|AF506288.1 **G** prokineticin receptor 2 [Homo sapiens]

dbj|BAC24022.1| **G** GPRg2 [Homo sapiens]

emb|CAI22379.1| **G** prokineticin receptor 2 [Homo sapiens]

gb|AAI04960.1| **G** Prokineticin receptor 2 [Homo sapiens]

gb|AAI04962.1| **G** Prokineticin receptor 2 [Homo sapiens]

Length=384

GENE ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 116 bits (291), Expect = 1e-25, Method: Compositional matrix adjust.  
Identities = 98/373 (26%), Positives = 173/373 (46%), Gaps = 41/373 (10%)

```
Query 16  SONGTNTTEATP-----ATNLTFPS-SYQHTSPV-----AAMPFIVAYAL- 52
+QNG NT TP A++L+F+ SY + P+ AA ++ AL
Sbjct 3  AQNG-NTSFTPNFNPPQDHASSLSFNFSYGDYDLPMEDEDMTKTRTFFAKIVIGIALA 61

Query 53  -IFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI--TGW 109
I L+C +GN+ + + + + +TN+ I NLA+SD LV I C P + + + W
Sbjct 62  GIMLVCGIGNFVFIAALTRYKKLRNLTNLLIANLAISDFLVAIICCFEMDYVVRQLSW 121

Query 110  PFDNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLTLRKALVTIAVIWALA 169
+ C ++ +S+ S L+AIA++R+ IVHP + ++ + A IA++W ++
Sbjct 122  EHGHLVCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLKPRMNYQTASFLIALVVMVS 181

Query 170  LLIMCPSAVTLTIVTREEHHFMVDARNRSYPLYSWEAWP--EKGMRVYTTVLFSHIYLA 227
+LI PSA T E F+V ++ + + C + WP ++ + Y +F ++
Sbjct 182  ILIATPSAYFAT---ETVLFIKVSQEKIF---CGIWPVDQQLYKSYFLFIFGVEFVG 234

Query 228  PLALIVVMYARIARKLCQAPGAPGGEAAADPRASRRRRVHVHMLVMVALFFTLWSLPLW 287
P+ + + YARI+R+L P E+ RR+ +V M ++ A + L W P +
Sbjct 235  PVVMTLCYARISRELWFKAVPGFQTEQIRKRLRCRRTVLVLMCILTA--YVLCWAPPY 292

Query 288  ALLLLIDYG-QLSAPQLHLVTYVYAFPAHWAFFNSSANPIIYGYNENFRRGFQAAPRA 346
++ D+ + + H+T AF +A NS N + + N + F+
Sbjct 293  GFTIVRDFPFTVFVKEKHYLT--AFYVVECIAMSNMINTVCFVTVKNTMKYFKKMMLL 350

Query 347  RLCPRPSGSHKEA 359
P GS A
Sbjct 351  HWRPSQRGSKSSA 363
```

>gb|EAX10422.1| **G** prokineticin receptor 2 [Homo sapiens]  
Length=811

GENE ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 116 bits (290), Expect = 2e-25, Method: Compositional matrix adjust.  
Identities = 85/324 (26%), Positives = 153/324 (47%), Gaps = 18/324 (5%)

```
Query 43  AAMPFIVAYAL--IFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTT 100
AA ++ AL I L+C +GN+ + + + + +TN+ I NLA+SD LV I C P
Sbjct 478  AAKIVIGIALAGIMLVCGIGNFVFIAALTRYKKLRNLTNLLIANLAISDFLVAIICCFE 537

Query 101  LVDNLIT- -GWFPDNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLTLRKA 158
+ + + + + C ++ +S+ S L+AIA++R+ IVHP + ++ + A
Sbjct 538  MDYVVRQLSWEHGHLVCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLKPRMNYQTA 597

Query 159  LVTIAVIWALALLIMCPSAVTLTIVTREEHHFMVDARNRSYPLYSWEAWP--EKGMRVY 216
IA++W +++LI PSA T E F+V ++ + + C + WP ++ + Y
Sbjct 598  SFLIALVVMVSILIAIPSAFAT---ETVLFIKVSQEKIF---CGIWPVDQQLYKSY 650

Query 217  TTVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGGEAAADPRASRRRRVHVHMLVMA 276
+F ++ P+ + + YARI+R+L P E+ RR+ +V M ++ A
Sbjct 651  FLFIIFGVFEFVGVVMTMLCYARISRELWFKAVPGFQTEQIRKRLRCRRTVLVLMCILTA 710

Query 277  LFFTLWSLPLWALLLLID-YGQLSAPQLHLVTYVYAFPAHWAFFNSSANPIIYGYNEN 335
+ L W P + ++ D + + + H+T AF +A NS N + + N
Sbjct 711  --YVLCWAPPYGFITVRDFPFTVFVKEKHYLT--AFYVVECIAMSNMINTVCFVTVKNN 766

Query 336  FRRGFQAAPRARLCPRPSGSHKEA 359
+ F+ P GS A
Sbjct 767  TMKYFKKMMLLHWRPSQRGSKSSA 790
```

>dbj|BAG36594.1| **G** unnamed protein product [Homo sapiens]  
Length=369

GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
(Over 10 PubMed links)

Score = 116 bits (290), Expect = 2e-25, Method: Compositional matrix adjust.  
Identities = 96/376 (25%), Positives = 172/376 (45%), Gaps = 44/376 (11%)

```
Query 1  MEGEPSQPPNS--SWPLSONGTNTTEATPATNLTFSSYYQHTSPVAAMPFIVAYALIFLLCM 58
M EP ++ S P NG+ +T +N T YY TS FI Y ++ + +
Sbjct 3  MADEPLNGSHTWLSIPFDLNGS-VVSTNTSNQT-EPYDLSNAVLTFI--YFVVCIIGL 58

Query 59  VGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLIITGWFPDNATCKM 118
GNTLV +++++ M T TN++ILNLA++D L + + P + + WPF A C++
Sbjct 59  CGNTLVIYVILRYAKMKTTTNIYILNLAIADELFLMLGLPFLAMQVALVHWPPGKAICRV 117

Query 119  SGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLTLR--KALVTIAVIWALALLIMCP 175
V G++ S+F L +++++R+ +VHP + R + +T+AV W ++LL++ P
Sbjct 118  VMTVNGINQFTSIFCLTVMSIDRYLAVVHPKSAKWRPRPTAKMITMAV-WGVSLVLILP 176

Query 176  SAVTLTIVTREEHHFMVDARNRSYPLYSWEAWPEKGMRRVYTTVLFSHI--YLAPLALIV 233
+ R+ + SC WP + +++++ I +L PL +I
Sbjct 177  IMI-----YAGLRNQWGRSSCTINWPGESGAWYTGPIIYTFILGLVPLTIIC 225

Query 234  VMYARIARKLCQAPGAPGGEAAADPRASRRRRVHVHMLVMVALFFTLWSLPLWALLLLI 293
+ Y I K+ G + + +V M+ +V F WLP + +
Sbjct 226  LCYLFIITKV-----KSSGIRVGSSKRKKSEKKVTRMVSIVVAVFIFCWLPFY----IF 275
```

Query 294 DYQQLS-----APQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAAF-RAR 347  
 + S P L + F F L + NS ANPI+Y + ++NF++ FQ +  
 Sbjct 276 NVSSVSMASPTPALKGM----PDFVVVLTANSKANPILYAFLLSDNFKKSQNVLCVK 331  
 Query 348 LCPRPSGSHKEAYSER 363  
 + G ++ ++  
 Sbjct 332 VSGTDDGERSDSKQDK 347

>gb|AAH95542.1| **G** Neuromedin B receptor [Homo sapiens]  
 Length=390

GENE ID: 4829 NMBR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 115 bits (289), Expect = 2e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)

Query 50 YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGW 109  
 Y LI + ++GN ++ I + N M +V N+FI NLA DLL+ + C+P W  
 Sbjct 50 YLLIITVGLLGNIMLVKIFITNSAMRSVPNIFISNLAAGDLLLLTCTVPVDASRYFFDEW 109  
 Query 110 PFDNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLT--LRKALVTIAVIWA 167  
 F CK+ ++Q SV SVFTL A++ +R+R IV+P + + L + V IW  
 Sbjct 110 MFGKVGCKLIPVIQLTSVGVSVFTLTALSADRYRAIVNPMQMOTSGALLRTCVKAMGIWV 169  
 Query 168 LALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCWEAWPEKGM--RVYTTVLFSHIY 225  
 ++L+ P AV V R + N S+ +C +P+ ++++ ++F +  
 Sbjct 170 VSVLLAVPEAVFSEVAR-----ISSLDNSSFT--ACI-PYPQTDELHPKIHSVLIFLVYF 221  
 Query 226 LAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALFFTLSWLP 285  
 L PLA+I + Y IA+ L ++ PG + R R+ ++++ F W P  
 Sbjct 222 LIPLAIISIYCHIAKLIKSAHNLPGEYNEHTKKQMETRKLAKIVLVFVGCFIFCWFP 281  
 Query 286 LWALLL--IDYQLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAA 343  
 L + +Y ++ H++ A L+F NS NP +E+FRF P  
 Sbjct 282 NHILYMYRSFNYNIDPSLGHMIVTLV---ARVLSFGNSCVNPFALYLLSESFRHFN-- 336  
 Query 344 FRARLCPRPSGSHKEAYSER 363  
 ++LC +++Y ER  
 Sbjct 337 --SQLC-----CGRKSYQER 349

>gb|ABQ52418.1| **G** prokineticin receptor 2 [Homo sapiens]  
 Length=384

GENE ID: 128674 PROKR2 | prokineticin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)

Score = 115 bits (289), Expect = 2e-25, Method: Compositional matrix adjust.  
 Identities = 98/373 (26%), Positives = 173/373 (46%), Gaps = 41/373 (10%)

Query 16 SQNGNTTEATP-----ATNLTFSS-SYYQHTSPV-----AAMPFIVAYAL- 52  
 +QNG NT TP A++L+P+ SY + P+ AA ++ AL  
 Sbjct 3 AQNG-NTSFTPNFNPQDHASSLSFNFSYGDYDLPMDEDEDMTKTRTPFAAKIVIGIALA 61  
 Query 53 -IFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI--TGW 109  
 I L+C +GN + + + + +TN+ I NLA+SD LV I C P + ++ W  
 Sbjct 62 GIMLVCGIGNVFVIAALTRYKKLRNLNLLIANLAISDFLVAICCPFEMDYVVRQLSW 121  
 Query 110 PFDNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLTLRKALVTIAVIWALA 169  
 + C ++ +S+ S L+AIA++R+ IVHP + ++ + A IA++W ++  
 Sbjct 122 EHGHVLCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPLKPRMNYQTASFLIALVWMVS 181  
 Query 170 LLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCWEAWP--EKGMRVYTTVLFSHIYLA 227  
 +LI PSA T E F+V ++ + + C + WP ++ + Y +F ++  
 Sbjct 182 ILIAIPSAIFAT---ETVLFIVKSQEKIF---CGQIWPVDQQLYKSYFLIFIGVEFVG 234  
 Query 228 PLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALFFTLSWLPW 287  
 P+ + + YARI+R+L P E+ RR+ +V M++ A + L W P +  
 Sbjct 235 PVVMTLTCYARISRELWFKAVPGFQTEQIRKRLRCRRKTVLVLMCILTA--YVLCWAPFY 292  
 Query 288 ALLLLIDYG-QLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAAFRA 346  
 ++ D+ + + H +T AF +A NS N + + N + F+  
 Sbjct 293 GFTIVRDFPPTVFVKEKHYLT--AFYVVECIAMSNMINTMCFVTVKNNTMKYFKKMMLL 350  
 Query 347 RLCPRPSGSHKEA 359  
 P GS A  
 Sbjct 351 HWRPSQRGSKSSA 363

>ref|NP\_002502.2| **G** neuromedin B receptor [Homo sapiens]

sp|P28336.2|NMBR\_HUMAN **G** RecName: Full=Neuromedin-B receptor; Short=NMB-R; AltName: Full=Neuromedin-B-preferring bombesin receptor

emb|CAH70473.1| **G** neuromedin B receptor [Homo sapiens]

gb|EAW47886.1| **G** neuromedin B receptor [Homo sapiens]  
 Length=390

GENE ID: 4829 NMBR | neuromedin B receptor [Homo sapiens]  
 (Over 10 PubMed links)

Score = 115 bits (288), Expect = 3e-25, Method: Compositional matrix adjust.  
 Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)

Query 50 YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGW 109  
 Y LI + ++GN ++ I + N M +V N+FI NLA DLL+ + C+P W  
 Sbjct 50 YLLIITVGLLGNIMLVKIFITNSAMRSVPNIFISNLAAGDLLLLTCTVPVDASRYFFDEW 109  
 Query 110 PFDNATCKMSGLVQGMVSASVFTLVIAIAVERFRCIVHPFREKLT--LRKALVTIAVIWA 167  
 F CK+ ++Q SV SVFTL A++ +R+R IV+P + + L + V IW  
 Sbjct 110 MFGKVGCKLIPVIQLTSVGVSVFTLTALSADRYRAIVNPMQMOTSGALLRTCVKAMGIWV 169  
 Query 168 LALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCWEAWPEKGM--RVYTTVLFSHIY 225  
 ++L+ P AV V R + N S+ +C +P+ ++++ ++F +  
 Sbjct 170 VSVLLAVPEAVFSEVAR-----ISSLDNSSFT--ACI-PYPQTDELHPKIHSVLIFLVYF 221



```

Query 226 LAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALFFTLISWLP 285
          L PLA+I + Y IA+ L ++ PG + R R+ ++++ F W P
Sbjct 222 LIPLAIIISIIYYHIAKTLIKSAHNLPGEYNEHTKKQMETRKRRLAKIVLVFVGCFIFCWFP 281

Query 286 LWALLLL--IDYQQLSAPQLHLVTYVYAPFFAHWLAFNSSANPIIYGYNENFRRGFQAA 343
          L + ++Y ++ H++ A L+F NS NP +E+FRR F
Sbjct 282 NHILYMYRSFNYNEIDPSLGHMIVTLV--ARVLSFGNSCVNPFALYLLSESFRRHFN-- 336

Query 344 FRARLCPRPSGSHKEAYSER 363
          ++LC +++Y ER
Sbjct 337 --SQLC-----CGRKSYQER 349

```

```

>gb|AAA59939.1| G neuromedin B receptor
gb|AAB27330.1| G neuromedin B receptor, NMB receptor=bombesin-like peptide receptor
[human, SCLC cell line H345, Peptide, 390 aa]
Length=390

```

```

GENE ID: 4829 NMBR | neuromedin B receptor [Homo sapiens]
(Over 10 PubMed links)

Score = 115 bits (288), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 89/320 (27%), Positives = 152/320 (47%), Gaps = 26/320 (8%)

```

```

Query 50 YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGW 109
          Y LI + ++GN ++ I + N M +V N+FI NLA DLL+ + C+P W
Sbjct 50 YLLIITVGLLGNIMLVKIFITNSAMRSVNPINIFISNLAAGDLLLLTLCVPVDASRYPFDEW 109

Query 110 PFDNATCKMSGLVQMSVSASVFTLVIAIAVERFCRIVHPFREKLT--LRKALVTIAVIWA 167
          F CK+ ++Q SV SVFTL A++ +R+R IV+P + + L + V IW
Sbjct 110 MFGKVGCKLIPVIQLTSVGVSVFTLTALSADRYRAIVNPMDMQTSGLLRCTCVKAMGIWV 169

Query 168 LALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSWEAWPEKGM--RVYTTVLFSHIY 225
          +++L+ P AV V R + N S+ +C +P+ +++ ++F +
Sbjct 170 VSVLLAVEAVFSEVAR-----ISSLDNSSFT--ACI-PYPQDELHPKIHSLIFLVYF 221

Query 226 LAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRARVHMLVMVALFFTLISWLP 285
          L PLA+I + Y IA+ L ++ PG + R R+ ++++ F W P
Sbjct 222 LIPLAIIISIIYYHIAKTLIKSAHNLPGEYNEHTKKQMETRKRRLAKIVLVFVGCFIFCWFP 281

Query 286 LWALLLL--IDYQQLSAPQLHLVTYVYAPFFAHWLAFNSSANPIIYGYNENFRRGFQAA 343
          L + ++Y ++ H++ A L+F NS NP +E+FRR F
Sbjct 282 NHILYMYRSFNYNEIDPSLGHMIVTLV--ARVLSFGNSCVNPFALYLLSESFRRHFN-- 336

Query 344 FRARLCPRPSGSHKEAYSER 363
          ++LC +++Y ER
Sbjct 337 --SQLC-----CGRKSYQER 349

```

```

>gb|AAA36623.1| G somatostatin receptor
dbj|BAA04106.1| G fourth somatostatin receptor subtype [Homo sapiens]
gb|AAS55648.1| G somatostatin receptor 4 [Homo sapiens]
gb|AAH69063.1| G Somatostatin receptor 4 [Homo sapiens]
gb|AAI17273.1| G Somatostatin receptor 4 [Homo sapiens]
Length=388

```

```

GENE ID: 6754 SSTR4 | somatostatin receptor 4 [Homo sapiens]
(Over 10 PubMed links)

Score = 115 bits (287), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

```

```

Query 50 YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGW 109
          YAL+ L+ +VGN I/V F++L+ M T TN++LNLAV+D L + +P + W
Sbjct 54 YALVCLVGLVGNALVIFVILRYAKMKTATNIYLLNLAVADELF-MLSVFPVASSAALRHW 112

Query 110 PFDNATCKMSGLVQMSVSASVFTLVIAIAVERFCRIVHPFREKLTIRKALVTIAV--IWA 167
          PF + C+ V G+++ SVF L ++V+R+ +VHP R R ++ + +W
Sbjct 113 PFGSVLCRAVLSDVGLNMFTSVFCLTVLSVDRIYAVVHPLRAATYRRRPSVAKLINLGVWL 172

Query 168 LALLIMCPSAVTLTVTREEHHFMDAR--NRSYPLYSWEAWPEKGMRRVYTTVLFSHIYL 226
          +LL+ P A+ D R R +C WP V+ F +L
Sbjct 173 ASLLVTLPIAI-----FADTRPARGGQAVACNLQWHPAWSAVVFVYTFLLGFL 221

Query 227 APLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRA--RVVHMLVMVALFFTLISWL 284
          P+ I + Y I K+ +A G ++ RRR+ ++ ++MV + F L W+
Sbjct 222 LPVLAIGLCYLLIIVGKM-RAVALRAGWQ-----RRRSEKITRLVLMVVVFPVLCWM 273

Query 285 PLWALLLL-IDYQQLSAPQLHLVTYVYAPFFAHWLAFNSSANPIIYGYNENFRRGFQAA 343
          P + + LL + L A H+ + L++ NS ANPI+YG+ ++NFRR FQ
Sbjct 274 PFYVQQLNLNVVTSLDATVNHVSLI-----LSYANSCANPILYGFLSDNFRRSFQRV 325

Query 344 FRARLC 349
          R C
Sbjct 326 LCLRCC 331

```

```

>gb|AAK61266.1|AE006466_1 G somatostatin receptor type 5 [Homo sapiens]
Length=364

```

```

GENE ID: 6755 SSTR5 | somatostatin receptor 5 [Homo sapiens]
(Over 10 PubMed links)

Score = 115 bits (287), Expect = 4e-25, Method: Compositional matrix adjust.
Identities = 93/307 (30%), Positives = 146/307 (47%), Gaps = 40/307 (13%)

```

```

Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFDNATCKMS 119
          GNTLV ++VL+ M TVTN++ILNLAV+D+L + +P N + WPF C++
Sbjct 57 GNTLVIYVVLRFAMKMTVTNIYILNLAVADVLY-MLGLPLATQNAASFVPFGLVLCRLV 115

Query 120 GLVQMSVSASVFTLVIAIAVERFCRIVHPFREKLTIRKALVTI--AVIWAALLIMCPSA 177
          + G++ SVF L ++V+R+ +VHP R + + A W L+L + P
Sbjct 116 MTLDGVNQFTSVFCLTVMSVDRIYAVVHPLSSARWRRPRVAKLASAAWVLSLCSLPLL 175

```

Query	178	VTLTVTREEHHFMDARNRSYPLYSCWEAWPE-----KGMRRVYTTVLFSHIYLAPLALI	232
		V V +C +WPE + +YT VL + APL +I	
Sbjct	176	VFADVQEGG-----TCNASWPEPVGLWGAVFIITYAVLG---FPAPLLVI	217
Query	233	VVMYARIARKLCQAPGPAPGGEAAADPRASRRRRARVVHMLVMVALFPTLSWLPLWALLLL	292
		+ Y I K+ A G R S R +V M+++V L F WLP + + ++	
Sbjct	218	CLCYLLIVVVKV----RAAGVRVGCVRRRSER--KVTRMVLVVVLVFGCWLPPFTVNIV	270
Query	293	IDYGQLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAARARLCPRP	352
		++ PQ + + F L++ NS ANP++YG+ ++NFR+ FQ LC R	
Sbjct	271	--NLAVALPQ-EPASAGLYFFVILSYANSCANPVLGYFLSDNFRQSFQKV----LCLRK	323
Query	353	SGSHKEA 359	
		K+A	
Sbjct	324	GSGAKDA 330	

>ref|NP\_005950.1| **UG** melatonin receptor 1B [Homo sapiens]  
 sp|P49286.1|MTR1B\_HUMAN **G** RecName: Full=Melatonin receptor type 1B; AltName: Full=Mel1b melatonin receptor; Short=Mel-1B-R  
 gb|AAC50612.1| **G** Mel1b-melatonin receptor  
 dbj|BAA92315.1| **G** melatonin 1b receptor [Homo sapiens]  
 gb|AAS00461.1| **G** melatonin receptor 1B [Homo sapiens]  
 gb|AAH69163.1| **G** Melatonin receptor 1B [Homo sapiens]  
 gb|EAW66891.1| **G** melatonin receptor 1B [Homo sapiens]  
 Length=362

GENE ID: 4544 MTR1B | melatonin receptor 1B [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 114 bits (285), Expect = 6e-25, Method: Compositional matrix adjust.  
 Identities = 94/313 (30%), Positives = 143/313 (45%), Gaps = 34/313 (10%)

Query	58	MVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPFNDATCK	117
		+VGN LV VL+NR + N+F+++LA++DL+V + P LV GW CK	
Sbjct	55	VVGNTLVLSVLRNRKLRNAGNLFVLSLADLVVAFYPPYLILVAIFYDGWALGEEHCK	114
Query	118	MSGLVQGSVSASVFTLVIAVERFRCIVHPFREKLTLRK--ALVTIAVIWALALLIMCP	175
		S V G+SV SVF + AIA+ R+ I H R+ + I +IW L ++ + P	
Sbjct	115	ASAFVMGLSVIGSVFNITAIINRYCYICHSMAYHRIYRRWHTPLHICLIWLLTVVALLP	174
Query	176	SAVTLTVTREEHHFMDARNRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVM	235
		+F V + +YSC + + + V+ H +L P+A++	
Sbjct	175	-----NFFVGSLEYDPRIYSC--TFIQTASTQYTAAVVVIH-FLLPIAVVSFC	219
Query	236	YARIARKLCQAPGPAPGGEAAADPRASRRRRARVVHMLVMVALF--FTLSWLPLWALLLLI	293
		Y RI + QA A + R + + + L M +F F + W PL + L +	
Sbjct	220	YLRVWVLVLQARRKA----KPESRLCLKPSDLRSFLTMFVVVFIFAICWAPLNCIGLAV	274
Query	294	DYG-QLSAPQLHLVTVYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQAARARLCPR-	351
		Q APQ + F ++ LA+FNS N I+YG N+NFR ++ A PR	
Sbjct	275	AINPQEMAPQ---IPEGLFVTSYLLAYFNSCLNAIVYGLLNQNFREYKRILLALWNPRIH	331
Query	352	-----PSGSHKEA 359	
		GSH E	
Sbjct	332	CIQDASKGSHAEG 344	

>gb|AAH09522.1|AAH09522 **G** Unknown (protein for IMAGE:3354783) [Homo sapiens]  
 Length=346

GENE ID: 6752 SSTR2 | somatostatin receptor 2 [Homo sapiens]  
 (Over 10 PubMed links)  
 Score = 114 bits (284), Expect = 9e-25, Method: Compositional matrix adjust.  
 Identities = 86/340 (25%), Positives = 158/340 (46%), Gaps = 40/340 (11%)

Query	35	YYQHTSVAMAFIYAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGI	94
		YY TS FI Y ++ ++ + GNTLV +++L+ M T+TN++ILNLA++D L +	
Sbjct	14	YYDLTSNAVLTFI--YFVVCIIIGLCGNTLVIIYVILRYAKMKTITNIYILNLAIDELF-M	70
Query	95	FCMPTTLVDNLITGWPFNDATCKMSGLVQGSVSASVFTLVIAVERFRCIVHPFREKLT	154
		+P + + + WPF A C++ V G++ S+F L +++R+ +VHP +	
Sbjct	71	LGLPFLAMQVALVHWPFGKAICRVVMTVDGINQFTSIFCLTVMSIDRYLAVVHPIKSAKW	130
Query	155	LR---KALVTIAVIWALALLIMCPSAVTLTVTREEHHFMDARNRSYPLYSCWEAWPEKG	211
		R ++T+AV W ++LL++ P + R+ + SC WP +	
Sbjct	131	RRPRTAKMITMAV-WGVSLLVILPIMI-----YAGLRSNQWGRSSCTINWPGES	178
Query	212	MRRVYTTVLFSHI--YLAPLALIVVMYARIARKLCQAPGPAPGGEAAADPRASRRRRARVV	269
		+++I +L PL +I + Y I K+ G + + +V	
Sbjct	179	GAWYTGPIIYTFILGFLVPLTIICLCYLFIIIKV-----KSSGIRVGSKRKKSEKKVT	232
Query	270	HMLVMVALFPTLSWLPLWALLLLIDYGQLS----APQLHLVTVYAFPPFAHWLAFFNSSA	324
		M+ +V F WLP + + + +S P L + F F L + NS A	
Sbjct	233	RMVSIIVAVFIFCWLPHY----IFNVSSVSMASPTPALKGM----FDFVVVLTYANSCA	284
Query	325	NPIIYGYNENFRRGFQAAR-RARLCPRPSGSHKEAYSER 363	
		NPI+Y + ++NF++ FQ ++ G ++ ++	
Sbjct	285	NPILYAFLSDNFKKSFQNVLCVKGSGTDDGERSDSKQDK 324	

>ref|NP\_001043.2| **UG** somatostatin receptor 4 [Homo sapiens]  
 sp|P31391.2|SSR4\_HUMAN **G** RecName: Full=Somatostatin receptor type 4; AltName: Full=SS4R  
 emb|CAB51953.1| **G** somatostatin receptor 4 [Homo sapiens]  
 gb|AAI17271.1| **G** Somatostatin receptor 4 [Homo sapiens]  
 gb|EAX10170.1| **G** somatostatin receptor 4, isoform CRA\_c [Homo sapiens]  
 Length=388  
 GENE ID: 6754 SSTR4 | somatostatin receptor 4 [Homo sapiens]

(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

```
Query 50 YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGW 109
Sbjct 54 YAL+ L+ +VGN LV F++L+ M T TN+++LNLAV+D L + +P + W
YALVCLVGLVGNALVIFVILRYAKMKTATNIYLLNLAVADELF-MLSVPFVASSAALRHW 112

Query 110 PFDNATCKMSGLVQMSVSASVFTLVIAIAVERFRFCIVHPFREKLTLRKALVTIAV--IWA 167
Sbjct 113 PFGSVLCRAVLSVDGLNMFTSVFCLTVLSVDRIYAVVHPLRAATYRRPSVAKLINLGVWL 172

Query 168 LALLIMCPSAVTLTVTREEHFMVDAR-NRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYL 226
Sbjct 173 ASLLVTLPIAI-----FADTRPARGGQAVACNLQWPHPAWSAVFVVYTFLLGFL 221

Query 227 APLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRA--RVVHMLVMVALFFTLISWL 284
Sbjct 222 LPVLAIGLCYLLIIVGKM-RAVALRAGWQQ-----RRRSEKITRLVLMVVVVFVLCWM 273

Query 285 PLWALLLL-IDYQLSAPQLHLVTYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFOAA 343
Sbjct 274 PFYVQQLNLNLFVTSLDATVNHVSLI-----LSYANSCANPILYGFLSDNFRFRFQRV 325

Query 344 FRARLC 349
Sbjct 326 LCLRCC 331
```

>gb|AAN87342.1| **G** DRG kappa 1 splice variant KOR 1A [Homo sapiens]  
Length=366

GENE ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 97/340 (28%), Positives = 164/340 (48%), Gaps = 40/340 (11%)

```
Query 8 PNSSWPLSQNGTNTTEATPATNLTFSSYYQHTSPVAAMFIVA-YALIFLLCMVGNTLVCF 66
Sbjct 23 PNSS + + PA HSP + I A Y+++F++ +VGN+LV F
PNSS---AGSEDAQLEPA-----HISPAIPVITAVSVFVVGVLVGNLVMF 68

Query 67 IVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWFPDNATCKMSGLVQMS 126
Sbjct 69 +++ M T TN++I NLA++D LV MP L+ WPF +A CK+ + +
VIIRYTKMKTATNIYIFNLALADALVTT-TMPFQSTVYLMNSWPFGDALCKIVISIDYYN 127

Query 127 VSASVFTLVIAIAVERFRFCIVHPFREKLTLR---KALVTIAIWAALALLIMCPSAVTLT 183
Sbjct 128 + S+FTL ++V+R+ + HP + L R KA + IW L+ + SA+ L T
MFTSITFTITMMSVDRIYAVCHPVK-ALDFRTPLKAKIINICIWLLSSSVGI-SAILVGGT 185

Query 184 REEHFMVDARNRSP--LYSCWEAWPEKGMRRVYTTVLFSHIYLAPLALIVVMYARIAR 241
Sbjct 186 + V + +P YS W+ + + +F ++ P+ +I+V Y +
KVREDVDVIECSLQFPDDDYSWWDLFMK-----ICVFIFAFVIVPLIIIVCYTLMIL 237

Query 242 KLCQAPGPAPGGEEAADPRASRRRARVVHMLVMVALFFTLISWLPLWALLLLIDYQLSAP 301
Sbjct 238 +L ++ G E R R+ +++V F + W P+ +L+ G S
RL-KSVRLLSGSRE---KDRNLRRITRLVLVVAVFVVCWTPIIHIFILVEALGSTSHS 291

Query 302 QLHLVTYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFQ 341
Sbjct 292 L + Y F L + NSS NPI+Y + +ENF+R F+
TAALSSYY---FCIALGYTNSSLNPIYAFLDENFKRCFR 328
```

>gb|EAX10169.1| **G** somatostatin receptor 4, isoform CRA\_b [Homo sapiens]  
Length=389

GENE ID: 6754 SSTR4 | somatostatin receptor 4 [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 92/306 (30%), Positives = 150/306 (49%), Gaps = 34/306 (11%)

```
Query 50 YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGW 109
Sbjct 54 YAL+ L+ +VGN LV F++L+ M T TN+++LNLAV+D L + +P + W
YALVCLVGLVGNALVIFVILRYAKMKTATNIYLLNLAVADELF-MLSVPFVASSAALRHW 112

Query 110 PFDNATCKMSGLVQMSVSASVFTLVIAIAVERFRFCIVHPFREKLTLRKALVTIAV--IWA 167
Sbjct 113 PF + C+ + V G+++ SVF L ++V+R+ +VHP R R ++ + +W
PFGSVLCRAVLSVDGLNMFTSVFCLTVLSVDRIYAVVHPLRAATYRRPSVAKLINLGVWL 172

Query 168 LALLIMCPSAVTLTVTREEHFMVDAR-NRSYPLYSCWEAWPEKGMRRVYTTVLFSHIYL 226
Sbjct 173 +LL+ P A+ D R R +C WP V+ F +L
ASLLVTLPIAI-----FADTRPARGGQAVACNLQWPHPAWSAVFVVYTFLLGFL 221

Query 227 APLALIVVMYARIARKLCQAPGPAPGGEEAADPRASRRRA--RVVHMLVMVALFFTLISWL 284
Sbjct 222 P+ I + Y I K+ +A G ++ RRR+ ++ +++MV + F L W+
LPVLAIGLCYLLIIVGKM-RAVALRAGWQQ-----RRRSEKITRLVLMVVVVFVLCWM 273

Query 285 PLWALLLL-IDYQLSAPQLHLVTYAFPPFAHWLAFFNSSANPIIYGYNENFRRGFOAA 343
Sbjct 274 P + + LL + L A H+ + L++ NS ANPI+YG+ ++NFRR FQ
PFYVQQLNLNLFVTSLDATVNHVSLI-----LSYANSCANPILYGFLSDNFRFRFQRV 325

Query 344 FRARLC 349
Sbjct 326 LCLRCC 331
```

>emb|CAH73066.1| **G** prolactin releasing hormone receptor [Homo sapiens]  
Length=370

GENE ID: 2834 PRLHR | prolactin releasing hormone receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 113 bits (283), Expect = 1e-24, Method: Compositional matrix adjust.  
Identities = 99/305 (32%), Positives = 152/305 (49%), Gaps = 25/305 (8%)

```
Query 60 GNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLI-TGWFPDNATCKM 118
```



```

Query 134 LVIAIAVERFRCIVHPPREKLTLRKALVTIAVIWALALLIMCPSAVTLTVTRE-EHHFMVD 192
Sbjct 61 LVLIAVERHQLIINPRGWRPNRHHAYVGVIAVIWVLA VASSLPFLIYQVMTDEPFQNVTLT 120

Query 193 ARNRSYPLYSCEAWPEKGMRRVYTTVLFSHIYLAFLALIVVMYARIARKL 243
Sbjct 121 AYKDK--YVCFDQPPSDSHRLSYTLLLVLYQYFGPLCFIFICYFKV-RKL 167

```

>gb|AAM21070.1|AF498922\_1 **G** opioid receptor kappa [Homo sapiens]

gb|AAA20985.1| **G** kappa opioid receptor

dbj|BAG35888.1| **G** unnamed protein product [Homo sapiens]

Length=380

GENE ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (276), Expect = 6e-24, Method: Compositional matrix adjust.  
Identities = 89/310 (28%), Positives = 154/310 (49%), Gaps = 26/310 (8%)

```

Query 38 HTSPVAAMFIVA-YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFC 96
Sbjct 53 H SP + I A Y+++F++ +VGN+LV F++++ M T TN++I NLA++D LV
HTSPAIPVIIITAVYSVVVGLVGNLSLVMFVIIRYTKMKTATNIYIFNLALADALVTT-T 111

Query 97 MPTTLVDNLITGWPFNDATCKMSGLVQMSVSASVFTLVIAIAVERFRCIVHPPREKLTLR 156
Sbjct 112 MP L+ WPF + CK+ + ++ S+FTL ++V+R+ + HP + L R
MPFQSTVYLMNSWPFGLVLCIKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVK-ALDFR 170

Query 157 ---KALVTIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYP--LYSCWEAWPEKG 211
Sbjct 171 TPLKAKIINICIWLLSSSVGI-SAILVGGTKVREDVDVIECSLQFPDDDYSWWDLFMK-- 227

Query 212 MRRVYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGGEAAADPRASRRRARVVHM 271
Sbjct 228 -----ICVFIFAFVIPVLIIIVCYTLMILRL-KSVRLLSGSRE-----KDRNLRRITRL 275

Query 272 LVMVALFFTLWSLPLWALLLLIDYQLSAPQLHLVTYVAFPPFAHWLAFFNSSANPIIYGY 331
Sbjct 276 +++V F + W P+ +L+ G S L + Y F L + NSS NPI+Y +
VLVVVAVFVVCWTPHIFILVEALGSTSHSTAALSSYY---FCIALGYTNSSSLNPILYAF 332

Query 332 FNENFRRGFQ 341
Sbjct 333 +ENF+R F+
LDENFKRCFR 342

```

>ref|NP\_000903.2| **UG** opioid receptor, kappa 1 [Homo sapiens]

sp|P41145.2|OPRK HUMAN **G** RecName: Full=Kappa-type opioid receptor; AltName: Full=KOR-1

gb|AAC50158.1| **G** kappa opioid receptor

gb|AAA63906.1| **G** kappa opioid receptor

gb|AAH99912.1| **G** Opioid receptor, kappa 1 [Homo sapiens]

gb|BAW86723.1| **G** opioid receptor, kappa 1 [Homo sapiens]

prf||2104381A kappa opioid receptor

Length=380

GENE ID: 4986 OPRK1 | opioid receptor, kappa 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (276), Expect = 7e-24, Method: Compositional matrix adjust.  
Identities = 89/310 (28%), Positives = 154/310 (49%), Gaps = 26/310 (8%)

```

Query 38 HTSPVAAMFIVA-YALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFC 96
Sbjct 53 H SP + I A Y+++F++ +VGN+LV F++++ M T TN++I NLA++D LV
HTSPAIPVIIITAVYSVVVGLVGNLSLVMFVIIRYTKMKTATNIYIFNLALADALVTT-T 111

Query 97 MPTTLVDNLITGWPFNDATCKMSGLVQMSVSASVFTLVIAIAVERFRCIVHPPREKLTLR 156
Sbjct 112 MP L+ WPF + CK+ + ++ S+FTL ++V+R+ + HP + L R
MPFQSTVYLMNSWPFGLVLCIKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPVK-ALDFR 170

Query 157 ---KALVTIAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYP--LYSCWEAWPEKG 211
Sbjct 171 TPLKAKIINICIWLLSSSVGI-SAILVGGTKVREDVDVIECSLQFPDDDYSWWDLFMK-- 227

Query 212 MRRVYTTVLFSHIYLAFLALIVVMYARIARKLCQAPGAPGGEAAADPRASRRRARVVHM 271
Sbjct 228 -----ICVFIFAFVIPVLIIIVCYTLMILRL-KSVRLLSGSRE-----KDRNLRRITRL 275

Query 272 LVMVALFFTLWSLPLWALLLLIDYQLSAPQLHLVTYVAFPPFAHWLAFFNSSANPIIYGY 331
Sbjct 276 +++V F + W P+ +L+ G S L + Y F L + NSS NPI+Y +
VLVVVAVFVVCWTPHIFILVEALGSTSHSTAALSSYY---FCIALGYTNSSSLNPILYAF 332

Query 332 FNENFRRGFQ 341
Sbjct 333 +ENF+R F+
LDENFKRCFR 342

```

>gb|AAN32829.1|AF441129\_1 **G** cholecystokinin-C receptor [Homo sapiens]

gb|AAK38351.1| **G** CCK-B/gastrin receptor variant [Homo sapiens]

Length=516

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (276), Expect = 8e-24, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

```

Query 44 AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMTTLVD 103
Sbjct 55 A+ I YA+IFL+ + GN L+ ++ +R + TVTN F+L+LAVSDLL+ + CMP TL+
AIRITLYAVIFPLMSVGNMLIIVVLGLSRRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLP 114

Query 104 NLITGWPFNDATCKMSGLVQMSVSASVFTLVIAIAVERFRCIVHPPREKL--TLRKALVT 161
Sbjct 104 NL+ + F CK + G+SVS S +LVAIA+ER+ I P + ++ T A

```

```


Sbjct 115 NLMGTFIFGTIVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174
Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLF 221
          I W L+ L+M P V V + C WP +R+ ++ +L
Sbjct 175 IVATWLLSGLLMVPYPVYTVVQPVGPRVL-----QCVHRWPSARVRQTWSVLLL 223
Query 222 SHIYLAPLALIVVMYARIARKL 243
          ++ P ++ V Y I+R+L
Sbjct 224 LLLFFIPGVVMAVAYGLISREL 245

Score = 43.9 bits (102), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 APGPAPGGEAAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYQGLSAPQLHL 305
          APGP G +++R VV ML+++ + F L WLP+++ + P H
Sbjct 380 APGPGSGSRPTQAKLLAKKR--VVRMLLVIVVFLCWLVPVYS---ANTWRAFDGPGGAHR 434
Query 306 VTVYA-PFPAHWLAFFNSSANPIIYGYNENFR 338
          A F H L++ ++ NP++Y + + FR+
Sbjct 435 ALSGAPISFIHLLSYASACVNPLVYCFMHRFRQ 468

```

```

>gb|EAW68734.1|  cholecystokinin B receptor, isoform CRA_a [Homo sapiens]
Length=516

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]
(Over 10 PubMed links)

Score = 110 bits (275), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)


Query 44 AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD 103
          A+ I YA+IPL+ + GN L+ ++ +R+ TVTN F+L+LAVSDLL+ + CMP TL+
Sbjct 55 ARITLYAVIFILMSVGGNMLIIVVLGSLRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLP 114
Query 104 NLITGWPFDNATCKMSGLVQMSVSASVFTLVIAIAVERFCRIVHPFREKL--TLRKALVT 161
          NL+ + F CK + G+SVS S +LVAIA+ER+ I P + ++ T A
Sbjct 115 NLMGTFIFGTIICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174
Query 162 IAVIWALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLF 221
          I W L+ L+M P V V + C WP +R+ ++ +L
Sbjct 175 IVATWLLSGLLMVPYPVYTVVQPVGPRVL-----QCVHRWPSARVRQTWSVLLL 223
Query 222 SHIYLAPLALIVVMYARIARKL 243
          ++ P ++ V Y I+R+L
Sbjct 224 LLLFFIPGVVMAVAYGLISREL 245

Score = 43.9 bits (102), Expect = 0.001, Method: Compositional matrix adjust.
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

Query 246 APGPAPGGEAAADPRASRRRARVVHMLVMVALFFTLWSLPLWALLLLIDYQGLSAPQLHL 305
          APGP G +++R VV ML+++ + F L WLP+++ + P H
Sbjct 380 APGPGSGSRPTQAKLLAKKR--VVRMLLVIVVFLCWLVPVYS---ANTWRAFDGPGGAHR 434
Query 306 VTVYA-PFPAHWLAFFNSSANPIIYGYNENFR 338
          A F H L++ ++ NP++Y + + FR+
Sbjct 435 ALSGAPISFIHLLSYASACVNPLVYCFMHRFRQ 468

```

```

>gb|EAX05261.1|  G protein-coupled receptor 103, isoform CRA_a [Homo sapiens]
Length=258


GENE ID: 84109 QRFRP | pyroglutamylated RFamide peptide receptor [Homo sapiens]
(10 or fewer PubMed links)



Score = 110 bits (274), Expect = 1e-23, Method: Compositional matrix adjust.
Identities = 62/181 (34%), Positives = 101/181 (55%), Gaps = 8/181 (4%)








Query 51 ALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWP 110
          LIF L + GN LV ++V +++ M TVTN+PI +LA+SDLL+ FC+P T+ N+ W
Sbjct 53 VLIFALALFGNALVFPVVTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNISDNWL 112
Query 111 FDNATCKMSGLVQMSVSASVFTLVIAIAVERFCRIVHPFREK--LTRKALVTIAVIWAL 168
          CKM VQ +V + T+ I AVER+ +VHPF+ K T R+A + V+W +
Sbjct 113 GGAFICKMVPFVQSTAVVTEILTMTICIAVERHQGLVHPFKMKWQYTNRRFTMLGVVWL 172
Query 169 ALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLF'SHIYLAP 228
          A+++ P + ++ F+ + + C E W +++YTT + ++L P
Sbjct 173 AVIVGSPMW-HVQQLKIKYDFLYEKEH-----ICCLEEWTSPVHQKIYTTFILVILFLLP 226
Query 229 L 229
          L
Sbjct 227 L 227

```

```

>ref|NP_795344.1|  cholecystokinin B receptor [Homo sapiens]

sp|P32239.1|GASR_HUMAN  RecName: Full=Gastrin/cholecystokinin type B receptor; Short=CCK-B
receptor; Short=CCK-BR; AltName: Full=Cholecystokinin-2
receptor; Short=CCK2-R
gb|AAA35660.1|  cholecystokinin receptor
10 more sequence titles

gb|AAA35657.1|  cholecystokinin-B/gastrin receptor
gb|AAC37528.1|  gastrin receptor
dbj|BAA02564.1|  cholecystokinin receptor [Homo sapiens]
gb|AAH00740.1|  Cholecystokinin B receptor [Homo sapiens]
dbj|BAA04759.2|  cholecystokinin-B receptor/gastrin receptor [Homo sapiens]
gb|AAP35435.1|  cholecystokinin B receptor [Homo sapiens]
gb|AAP84364.1|  cholecystokinin B receptor [Homo sapiens]
Length=447

```

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 110 bits (274), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

```
Query 44  AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD 103
A+ I YA+IFL+ + GN L+ ++ +R + TVTN F+L+LAVSDLL+ + CMP TL+
Sbjct 55  ATRITLYAVIFMSVGGNMLIIVLGLSRRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLP 114

Query 104 NLITGWPPDNATCKMSGLVQMSVSASVFTLVIAIAVERFRCIVHPFREKL--TLRKALVT 161
NL+ + F CK + G+SVS S +LVAIA+ER+ I P + ++ T A
Sbjct 115 NLMGTFFIFGTVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174


Query 162 IAVIWAALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLF 221
I W L+ L+M P V V + C WP +R+ ++ +L
Sbjct 175 IVATWLLSGLLMVPYPVYTVVQPVGPRVL-----QCVHRWPSARVRQTWSVLLL 223

Query 222 SHIYLAPLALIVVMYARIARKL 243
++ P ++ V Y I+R+L
Sbjct 224 LLLFFIPGVVMAVAYGLISREL 245
```

Score = 44.3 bits (103), Expect = 7e-04, Method: Compositional matrix adjust.  
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)

```
Query 246 APGPAPGGEEAADPRASRRRARVHMLVMVALFFTLSWLPLWALLLLIDYQLSAPQLHL 305
APGP G ++R VV ML+++ + F L WLP+++ + P H
Sbjct 311 APGPSSGSRPTQAKLLAKKR--VVRMLLVIVVLFFLCWLPVYS---ANTWRAFDGPGAHR 365

Query 306 VTUYA-FPFAHWLAFNSSANPIIYGYPNENFRR 338
A F H L+++ NP++Y + + FR+
Sbjct 366 ALSGAPISFIHLLSYASACVNPLVYCFMHRFRQ 399
```

>gb|AAB30766.2|  cholecystokinin B receptor [Homo sapiens]  
Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 109 bits (273), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

```
Query 44  AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD 103
A+ I YA+IFL+ + GN L+ ++ +R + TVTN F+L+LAVSDLL+ + CMP TL+
Sbjct 55  ATRITLYAVIFMSVGGNMLIIVLGLSRRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLP 114

Query 104 NLITGWPPDNATCKMSGLVQMSVSASVFTLVIAIAVERFRCIVHPFREKL--TLRKALVT 161
NL+ + F CK + G+SVS S +LVAIA+ER+ I P + ++ T A
Sbjct 115 NLMGTFFIFGTVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174

Query 162 IAVIWAALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLF 221
I W L+ L+M P V V + C WP +R+ ++ +L
Sbjct 175 IVATWLLSGLLMVPYPVYTVVQPVGPRVL-----QCVHRWPSARVRQTWSVLLL 223


Query 222 SHIYLAPLALIVVMYARIARKL 243
++ P ++ V Y I+R+L
Sbjct 224 LLLFFIPGVVMAVAYGLISREL 245
```

Score = 44.7 bits (104), Expect = 7e-04, Method: Compositional matrix adjust.  
Identities = 26/94 (27%), Positives = 46/94 (48%), Gaps = 6/94 (6%)


```
Query 246 APGPAPGGEEAADPRASRRRARVHMLVMVALFFTLSWLPLWALLLLIDYQLSAPQLHL 305
APGP G ++R VV ML+++ + F L WLP+++ + P H
Sbjct 311 APGPSSGSRPTQAKLLAKKR--VVRMLLVIVVLFFLCWLPVYS---ANTWRAFDGPGAHR 365


Query 306 VTUYA-FPFAHWLAFNSSANPIIYGYPNENFRR 338
A F H L+++ NP++Y + + FR+
Sbjct 366 ALSGAPISFIHLLSYASACVNPLVYCFMHRFRQ 399
```


>ref|NP\_001040.1|  somatostatin receptor 1 [Homo sapiens]

sp|P30872.1|SSR1 HUMAN  RecName: Full=Somatostatin receptor type 1; AltName: Full=SS1R;  
AltName: Full=SRIF-2  
9 more sequence titles

gb|AAA58247.1|  somatostatin receptor isoform 1

gb|AAH35618.1|  Somatostatin receptor 1 [Homo sapiens]

gb|AAP84349.1|  somatostatin receptor 1 [Homo sapiens]

gb|EAW65836.1|  somatostatin receptor 1 [Homo sapiens]  
Length=391

GENE ID: 6751 SST1 | somatostatin receptor 1 [Homo sapiens]  
(Over 10 PubMed links)

Score = 109 bits (273), Expect = 1e-23, Method: Compositional matrix adjust.  
Identities = 87/330 (26%), Positives = 160/330 (48%), Gaps = 44/330 (13%)

```
Query 16  SQNGTNTATPATNLTFSSYYQHTSPVAAAMFIVAYALIFLLCMVGNTLVCFIVLKNRHM 75
SQNGT +E S + FI Y+++ L+ + GN++V +++L+ M
Sbjct 46  SQNGTLSEG-----QGSAILISFI--YSVVCLVGLCGNSMVIYVILRYAKMK 90

Query 76  TVTNMFILNLAVSDLLVGIFCMPTTLVDNLITGWPPDNATCKMSGLVQMSVSASVFTLV 135
T TN++ILNLAA++D L+ + +P + L+ WPF C++ V +++ S++ L
Sbjct 91  TATNIYIILNLAIADLEL-MLSVPFLVTSTLLRHWPFGALLCRLVLSVDVNMFTSIYCLT 149

Query 136 AIAVERFRCIVHPFREKLTLRKALVTIAV--IWAALLIMCPSAVTLTVTREEHHFMVDA 193
++V+R+ +VHP + R + + +W L+LL++ P V F A
Sbjct 150  VLSVDRYAVVHPKAAARYRRPTVAKVNVNLGVVLSLLVILPIV-----FSRTA 199

Query 194 RNRSYPLYSCWEAWPEKGMRRVYTTVLFHSI--YLAPLALIVVMYARIARKLCQAPGPAP 251
N S +C PE R + VL++ + +L P+ I + Y I K+
```

```

Sbjct 200 AN-SDGTVACNMLMPEPAQRWLVGFLVLYTFLMGFLLPVGAICLCYVLIIAKMRMV----- 253
Query 252 GGEEAADPRASRRRARVVHMLVMVALFFTLFWLPLWALLLLIDYQQLSAPQLHLVTVYAF 311
      +A + R ++ M++MV + F + W+P + + L+ + + + +V
Sbjct 254 -ALKAGWQQRKRSEKRTLMVMMVMVMFVICWMPFYVVQLVNVFAEQDDATVSQLSVI-- 310
Query 312 PFAHWLAFFNSSANPIIYGYPNENFRRGFQ 341
      L + NS ANPI+YG+ ++NF+R FQ
Sbjct 311 -----LGYANSCANPILYGFLSDNPKRSFQ 335

```

>gb|EAW68735.1| **G** cholecystokinin B receptor, isoform CRA\_b [Homo sapiens]  
Length=447

GENE ID: 887 CCKBR | cholecystokinin B receptor [Homo sapiens]  
(Over 10 PubMed links)

Score = 109 bits (273), Expect = 2e-23, Method: Compositional matrix adjust.  
Identities = 69/202 (34%), Positives = 107/202 (52%), Gaps = 13/202 (6%)

```

Query 44 AMFIVAYALIFLLCMVGNTLVCFIVLKNRHMHTVTNMFILNLAVSDLLVGIFCMPTTLVD 103
      A+ I YA+IFL+ + GN L+ ++ +R + TVTN F+L+LAVSDLL+ + CMP TL+
Sbjct 55 AIRITLYAVIFLMSVGGNMLIIIVLGLSRRLRTVTNAFLLSLAVSDLLAVACMPFTLLP 114
Query 104 NLITGWPPDNATCKMSGLVQGMSSASVFTLVAVIAVERFRCIVHPFREKL--TLRKALVT 161
      NL+ + F CK + G+SVS S +LVAIA+ER+ I P + ++ T A
Sbjct 115 NLMTGFIFGTIICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARV 174
Query 162 IAVIWAALALLIMCPSAVTLTVTREEHHFMVDARNRSYPLYSCWEAWPEKGMRRVYTTVLF 221
      I W L+ L+M P V V + C WP +R+ ++ +L
Sbjct 175 IVATWLLSGLLMVPYPVYTVVQPVGPRVL-----QCVHRWPSARVRQTWSVLLL 223
Query 222 SHIYLAPLALIVVMYARIARKL 243
      ++ P ++ V Y I+R+L
Sbjct 224 LLLFFIPGVVMAVAYGLISREL 245

```

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